

SEARCH REQUEST FORM

Requestor's
Name:

GAMBEL

Serial

Number:

08/487283

Date:

5/27/97

Phone:

308.3997

Art Unit:

1806

Search Topic:

Please write a detailed statement of search topic. Describe specifically as possible the subject matter to be searched. Define any terms that may have a special meaning. Give examples or relevant citations, authors keywords, etc., if known. For sequences, please attach a copy of the sequence. You may include a copy of the broadest and/or most relevant claim(s).

SEARCH SEQ ID NO. 1

① SEARCH INPUTS

② COMPLEMENT AND C5

③ ① + ② PRINT

④ ② + ALPHA (u) CHAIN ON (ANTI^(u)C5)

⑤ ④ + ANTIBOD? PRINT IF NOT TOO MUCH

⑥ IF ⑤ IS TOO MUCH, ADD (INHIBIT? OR SUPPRESS?)
PRINTREQUEST
FOR
THREATmy search place
Ten out till Aug 4
Shirley

STAFF USE ONLY

Date completed:

7-29-97

Searcher:

AGX

Terminal time:

Elapsed time:

CPU time:

Total time:

Number of Searches:

Number of Databases:

Search Site

STIC

CM-1

Pre-S

Type of Search

N.A. Sequence

A.A. Sequence

Structure

Bibliographic

Vendors

IG Suite

STN

Dialog

APS

Geninfo

SDC

DARC/Questel

Other

(TW)

Release 2.1D John F. Collins, BioComputing Research Unit.

Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K.

Distribution rights by Intelligenetics, Inc.

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Tue Jul 29 07:31:34 1997; MasPar time 3.22 Seconds
 Tabular output not generated. 188.119 Million cell updates/sec

Title: >US-08-487-283A-1
 Description: (1-21) from US08487283A.pep
 Perfect Score: 141
 Sequence: 1 VIDHGTSSKCKVRKVEGSS 21

Scoring table: PAM 150
 Gap 15

Searched: 91006 seqs, 2888923 residues

Post-processing: Minimum Match 0%
 Listing first 100 summaries

Database: pir51
 1:ann1 2:ann2 3:ann3 4:ann4 5:ann11 6:ann22 7:unann3
 8:unann4 9:unann5 10:unann6 11:unann7 12:unann8
 13:unann9 14:unann10 15:unenc 16:unrev

Statistics: Mean 25.430; Variance 35.904; scale 0.708

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	141	100.0	1676	2	C5HU	1.30e-19
2	69	48.9	1680	2	complement C5 precu	1.21e-02
3	59	41.8	940	9	lactoferrin binding	1.09e+00
4	59	41.8	1002	12	yemanuclein-alpha -	1.09e+00
5	58	41.1	205	14	protein tyrosine pho	1.68e+00
6	58	41.1	223	14	protein tyrosine pho	1.68e+00
7	57	40.4	117	13	ribosomal protein L3	2.56e+00
8	57	40.4	264	16	N-carbamoylsarcosine	2.56e+00
9	56	39.7	537	11	spore coat protein S	3.89e+00
10	56	39.7	540	11	vicilin-like storage	3.89e+00
11	56	39.7	573	11	globulin-1S, GLB1S -	3.89e+00
12	55	39.0	775	13	transposable element	5.88e+00
13	54	38.3	148	10	spore coat peptide C	8.85e+00
14	54	38.3	224	10	bioflavin-specific	8.85e+00
15	54	38.3	562	16	P element - fruit fl	8.85e+00
16	54	38.3	818	5	hypotheical protein	8.85e+00
17	54	38.3	841	1	dipterydyl aninopept	8.85e+00
18	54	38.3	1030	12	probable membrane pr	8.85e+00
19	53	37.6	116	4	early E4 11K protein	1.33e+01
20	53	37.6	116	4	early E4 11K protein	1.33e+01
21	53	37.6	148	7	glycine-rich RNA-bin	1.33e+01

epithelin/granulin p 1.33e+01
 omega-crystallin - g 1.33e+01
 galactosylceramidase 1.33e+01
 platelet-derived gro 1.33e+01
 TMV resistance prote 1.33e+01
 cell-fate determinin 1.33e+01
 globulin-0 protein - mai 1.97e+01
 globulin-10, GLB10 - 1.97e+01
 VSG expression site- 1.97e+01
 ornithine cyclodeami 1.97e+01
 methyiaspartate ammo 1.97e+01
 vicilin-like storage 1.97e+01
 pol polyprotein - fr 1.97e+01
 ribosomal protein L3 2.92e+01
 ribosomal protein L3 2.92e+01
 hypotheical protein 2.92e+01
 hypotheical protein 2.92e+01
 alcohol dehydrogenas 2.92e+01
 pyruvate kinase (EC 2.92e+01
 major envelope glyco 2.92e+01
 estrogen receptor - 2.92e+01
 granulin - rat 2.92e+01
 epithelin/granulin p 2.92e+01
 tracheobronchial muc 2.92e+01
 hypotheical protein 2.92e+01
 protein-tyrosine kin 2.92e+01
 protein-tyrosine kin 2.92e+01
 retrovirus-related p 2.92e+01
 vitellogenin 6 precu 2.92e+01
 clathrin heavy chain 2.92e+01
 ribosomal protein L1 4.30e+01
 hypotheical protein 4.30e+01
 D-ribose-binding pro 4.30e+01
 D-ribose-binding pro 4.30e+01
 troponin T, cardiac 4.30e+01
 mucin - human 4.30e+01
 benzene 1,2-dioxygen 4.30e+01
 hypotheical protein 4.30e+01
 hypotheical protein 4.30e+01
 beta-fructofuranosid 4.30e+01
 beta-fructofuranosid 4.30e+01
 Wnt-5 protein - frui 4.30e+01
 botulinum neurotoxin 4.30e+01
 serine proteinase in 6.29e+01
 variant surface glyc 6.29e+01
 zinc finger protein 6.29e+01
 hypotheical protein 6.29e+01
 ribosomal protein L1 6.29e+01
 antistatin - Hydra m 6.29e+01
 phage shock protein 6.29e+01
 hypotheical protein 6.29e+01
 probable membrane pr 6.29e+01
 developmental contro 6.29e+01
 nucleocapsid protein 6.29e+01
 steroid receptor hom 6.29e+01
 platelet-derived gro 6.29e+01
 beta-fructofuranosid 6.29e+01
 isomerase fuci (EC 5 6.29e+01
 Drosophila vasa homo 6.29e+01
 potassium channel pr 6.29e+01
 tral protein - Esche 6.29e+01
 transcription repres 6.29e+01
 platelet-derived gro 6.29e+01
 NMDA receptor subuni 6.29e+01
 NMDA receptor subuni 6.29e+01
 N-methyl-D-aspartate 6.29e+01
 N-methyl-D-aspartate 6.29e+01
 alpha-2 macroglobuli 6.29e+01
 hypotheical protein 9.15e+01
 hypotheical protein 9.15e+01
 probable helicase - 9.15e+01
 hypotheical protein 9.15e+01

589 7 C38128 37.6
 591 12 S43428 37.6
 669 13 I54205 37.6
 1089 1 PFHUGA 37.6
 1144 16 A54810 37.6
 2471 14 A49128 36.9
 122 11 S21823 36.9
 122 11 C53234 36.9
 329 3 VMUT21 36.9
 354 2 DURG0 36.9
 354 6 S55582 36.9
 582 11 B53234 36.9
 982 12 S00954 36.9
 121 7 S48427 36.2
 121 7 S53549 36.2
 238 8 S23314 36.2
 250 8 S07237 36.2
 337 5 A35260 36.2
 462 5 S29004 36.2
 529 4 VGNVAC 36.2
 574 7 A37197 36.2
 588 14 I53272 36.2
 589 7 B38128 36.2
 1056 13 A53767 36.2
 1084 8 S23319 36.2
 1129 14 A47511 36.2
 1132 14 JC4127 36.2
 1291 8 S05465 36.2
 1651 7 B43081 36.2
 1678 7 S52588 36.2
 123 7 F64093 35.5
 171 11 S56787 35.5
 271 4 JGEBRT 35.5
 296 4 JGECR 35.5
 302 3 TPCHTC 35.5
 313 13 S44474 35.5
 410 1 JN0810 35.5
 419 9 S51715 35.5
 547 11 S61032 35.5
 592 5 JQ0991 35.5
 592 16 S61503 35.5
 1004 12 A48821 35.5
 1268 6 S33411 35.5
 63 16 S21120 34.8
 72 7 S07254 34.8
 114 13 A45193 34.8
 174 10 E64467 34.8
 122 7 S15437 34.8
 220 16 S29195 34.8
 222 9 S17121 34.8
 313 11 S61990 34.8
 384 12 S66758 34.8
 424 14 S15917 34.8
 429 4 VHVUHV 34.8
 487 12 A46146 34.8
 491 5 S33767 34.8
 573 5 S49266 34.8
 591 2 ISECFI 34.8
 637 14 I49638 34.8
 660 14 S24125 34.8
 732 9 S23001 34.8
 784 13 A33633 34.8
 1088 1 PFRTGA 34.8
 1323 14 I78557 34.8
 1323 14 I58158 34.8
 1323 7 S27224 34.8
 1356 7 C42519 34.8
 1451 6 B41185 34.8
 1476 6 B41185 34.8
 117 11 S67845 34.0
 229 16 S30486 34.0
 360 16 A49600 34.0
 519 8 S38921 34.0

```

95 48 34.0 845 1 JDVLVD DNA-directed DNA pol 9.15e+01
96 48 34.0 925 5 A39216 plasma cell membrane 9.15e+01
97 48 34.0 948 8 A56602 glycoprotein B homol 9.15e+01
98 48 34.0 953 12 S55156 probable membrane pr 9.15e+01
99 48 34.0 1216 11 S46177 probable Ca2+-transp 9.15e+01
100 48 34.0 1299 12 S06119 membrane protein pat 9.15e+01

```

ALIGNMENTS

```

1
RESULT 1
ENTRY C5HU #type complete
TITLE complement C5 precursor - human
CONTAINS C5a anaphylatoxin; C5b
ORGANISM #formal_name Homo sapiens #common_name man
DATE 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change
ACCESSIONS A40075; A27689; A01267; A01266
REFERENCE A40075
#authors Haviland, D.L.; Haviland, J.C.; Fleischer, D.T.; Hunt, A.; Wetsel, R.A.
#journal J. Immunol. (1991) 146:362-368
#title Complete cDNA sequence of human complement pro-C5. Evidence of truncated transcripts derived from a single copy gene.
#cross-references MUID:91079575
#accession A40075
#molecule_type mRNA
#residues_type 1-1676 ##label HAV
#cross-references GB:M57129
#note 518-Ser was also found
REFERENCE A27689
#authors Wetsel, R.A.; Lemons, R.S.; Le Beau, M.M.; Barnum, S.R.; Noack, D.; Tack, B.F.
#journal Biochemistry (1988) 27:1474-1482
#title Molecular analysis of human complement component C5: localization of the structural gene to chromosome 9.
#cross-references MUID:88209511
#accession A27689
#molecule_type mRNA
#residues_type 412-1676 ##label WET
#cross-references GB:M18879
REFERENCE A01267
#authors Fernandez, H.N.; Hugli, T.E.
#journal J. Biol. Chem. (1978) 253:6955-6964
#title Primary structural analysis of the polypeptide portion of human C5a anaphylatoxin. Polypeptide sequence determination and assignment of the oligosaccharide attachment site in C5a.
#cross-references MUID:79005687
#accession A01267
#molecule_type protein
#residues_type 678-751 ##label FER
REFERENCE A01266
#authors Lundwall, A.B.; Wetsel, R.A.; Kristensen, T.; Whitehead, A.S.; Woods, D.E.; Ogden, R.C.; Colten, H.R.; Tack, B.F.
#journal J. Biol. Chem. (1985) 260:2108-2112
#title Isolation and sequence analysis of a cDNA clone encoding the fifth complement component.
#cross-references MUID:85130937
#accession A01266
#molecule_type mRNA
#residues_type 412-854,
#label LUN
#cross-references GB:K02874
#note the carboxyl-terminal part of the sequence in this report appears to be derived from translation of an ALU repeat sequence
COMMENT Complement C5 contains two disulfide-linked chains, formed by removal of four basic residues. C5 convertase releases C5a anaphylatoxin from the amino end of the alpha chain, generating C5b (beta and alpha' chains).
COMMENT Activation of C5 initiates the spontaneous assembly of the late

```

```

complement components, C5-C9, into the membrane attack complex.
C5b has a transient binding site for C6. The C5b-C6 complex is
the foundation upon which the membrane attack complex is
assembled.
COMMENT C5a has potent spasmogenic and chemotactic activity.
GENETICS
#gene GDB:C5
#cross-references GDB:119734
#map_position 9q33-q33
CLASSIFICATION #superfamily alpha-2-macroglobulin
KEYWORDS complement alternate pathway; complement pathway; cytolysis;
glycoprotein; inflammatory response; membrane attack
complex; plasma

```

```

FEATURE
1-18
19-673, 678-1676 #domain signal sequence #status predicted #label SIG\
19-673, 752-1676 #product C5b #status predicted #label MAT\
19-673 #product complement C5 and C5b beta chain #status
predicted #label C5BA\
678-1676 #product complement C5 alpha chain #status predicted
#label C5A\
678-751 #product C5a anaphylatoxin #status experimental #label
C5A\
752-1676 #product C5b alpha' chain #status predicted #label C5BA\
567-810, 634-669,
698-724, 699-731,
711-732, 866-1527,
1101-1159,
1375-1505,
1405-1474,
1520-1525,
1532-1606,
1553-1676,
1634-1657,
741
751-752
911, 1115, 1630

```

```

#disulfide_bonds #status predicted\
#binding_site carbohydrate (Asn) (covalent) #status
experimental\
#cleavage_site Arg-Leu (C5 convertase) #status
experimental\
#binding_site carbohydrate (Asn) (covalent) #status
predicted
SUMMARY #length 1676 #molecular_weight 188330 #checksum 3858
Query Match 100.0%; Score 141; DB 2; Length 1676;
Best Local Similarity 100.0%; Pred. No. 1.30e-19;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Db 872 vidhgtksskcvrkvegss 892
|||||
QY 1 VIDHGTSSKCVRKVEGSS 21
|||||
RESULT 2
ENTRY #type complete
TITLE complement C5 precursor - mouse
CONTAINS C5a anaphylatoxin; C5b
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE 19-Nov-1988 #sequence_revision 15-Oct-1994 #text_change
15-Oct-1994
ACCESSIONS A35530; A27538; A40429
REFERENCE A35530
#authors Wetsel, R.A.; Fleischer, D.T.; Haviland, D.L.
#journal J. Biol. Chem. (1990) 265:2435-2440
#title Deficiency of the murine fifth complement component (C5). A
2-base pair gene deletion in a 5'-exon.
#cross-references MUID:90153853
#accession A35530
#molecule_type mRNA
#residues_type 1-215, 'L' ##label WET
#cross-references GB:J05234
REFERENCE A27538
#authors Wetsel, R.A.; Ogata, R.T.; Tack, B.F.
#journal Biochemistry (1987) 26:737-743
#title Primary structure of the fifth component of murine

```

```

ENTRY      S49087      #type complete
TITLE      lactoferrin binding protein - Neisseria meningitidis
ORGANISM   #formal_name Neisseria meningitidis
DATE       16-Feb-1995 #sequence_revision 12-May-1995 #text_change
12-May-1995

ACCESSIONS S49087
REFERENCE   S49087
AUTHORS    Pettersson, A.M.; Klarenbeek, X.Y.Z.; van Deurzen, X.Y.Z.;
Poolman, X.Y.Z.; Tommassen, X.Y.Z.
#submission Submitted to the EMBL Data Library, June 1994
#description Molecular characterization of the structural gene for the
lacto-ferrin receptor of the meningococcal strain H44/76.

#accession S49087
#status preliminary
#molecule_type DNA
#residues 1-940 #label pET
#cross-references EMBL:X79838

SUMMARY    #length 940 #molecular-weight 105347 #checksum 8194

Query Match 41.8%; Score 59; DB 9; Length 940;
Best Local Similarity 50.0%; Pred. No. 1.09e+00;
Matches 7; Conservative 5; Mismatches 2; Indels 0; Gaps 0

Db 592 rsrkcvcprkingsn 605
:| ||| :|||:
QY 8 KSSKCVQRKVEGSS 21

RESULT     4
ENTRY      A56678      #type complete
TITLE      ymanuclein-alpha - fruit fly (Drosophila melanogaster)
ORGANISM   #formal_name Drosophila melanogaster
DATE       08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change
11-Aug-1995

ACCESSIONS A56678; S22146
REFERENCE   A56678
AUTHORS    Ali-Ahmed, O.; Bellon, B.; Capri, M.; Joblet, C.;
Thomas-Delaage, M.
#journal   Mech. Dev. (1992) 37:69-80
#title     The ymanuclein-alpha: a new Drosophila DNA binding protein
specific for the oocyte nucleus.

#accession A56678
#status preliminary
#molecule_type DNA
#residues 1-1002 #label AIE
#cross-references GB:X63503

GENETICS
#introns 80/3; 154/3; 428/1 477/2; 557/2
KEYWORDS   DNA binding; oocyte
SUMMARY    #length 1002 #molecular-weight 109310 #checksum 4278

Query Match 41.8%; Score 59; DB 12; Length 1002;
Best Local Similarity 50.0%; Pred. No. 1.09e+00;
Matches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0

Db 47 tktakcirikld 58
||::|||:|::
QY 7 TKSSKCVQRKVE 18

RESULT     5
ENTRY      I49364      #type complete
TITLE      protein tyrosine phosphatase - mouse
ORGANISM   #formal_name Mus musculus #common_name house mouse
DATE       02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
02-Jul-1996

ACCESSIONS I49364
REFERENCE   I49364
AUTHORS    Wishart, M.J.; Denu, J.M.; Williams, J.A.; Dixon, J.E.
#journal   J. Biol. Chem. (1995) 270:26782-26785
#title     A single mutation converts a novel-phosphotyrosine binding
domain into a dual-specificity phosphatase.

#accession I49364

```

```

##status      preliminary; translated from GB/EMBL/DBDJ
##molecule_type  mRNA
##residues      1-205 ##label RES
##cross-references  EMBL:U34973; NID:g1063624; CDS_PID:g1063625
SUMMARY          #length 205 #molecular-weight 23693 #checksum 2745

Query Match      41.1%; Score 58; DB 14; Length 205;
Best Local Similarity 25.0%; Pred. No. 1.68e+00;
Matches          5; Conservative 9; Mismatches 6; Indels 0; Gaps 0;

Db 51 liqkghithicirngnean 70
   :::| |::|::|::
QY 1 VIDHGTGKSKCVROKVEGS 20

RESULT 6
ENTRY   I49365      #type complete
TITLE   protein tyrosine phosphatase - mouse
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE     02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
02-Jul-1996
ACCESSIONS I49365
REFERENCE  I49364
#authors   Wishart, M.J.; Denu, J.M.; Williams, J.A.; Dixon, J.E.
#journal   J. Biol. Chem. (1995) 270:26782-26785
#title     A single mutation converts a novel-phosphotyrosine binding
           domain into a dual-specificity phosphatase.
#accession I49365
##status   preliminary; translated from GB/EMBL/DBDJ
##molecule_type  mRNA
##residues      1-223 ##label RES
##cross-references  EMBL:U34973; NID:g1063624; CDS_PID:g1063626
GENETICS  168/3
#introns    #length 223 #molecular-weight 25416 #checksum 359

Query Match      41.1%; Score 58; DB 14; Length 223;
Best Local Similarity 25.0%; Pred. No. 1.68e+00;
Matches          5; Conservative 9; Mismatches 6; Indels 0; Gaps 0;

Db 51 liqkghithicirngnean 70
   :::| |::|::|::
QY 1 VIDHGTGKSKCVROKVEGS 20

RESULT 7
ENTRY   I68524      #type complete
TITLE   ribosomal protein L34 - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE     24-May-1996 #sequence_revision 24-May-1996 #text_change
24-May-1996
ACCESSIONS I68524
REFERENCE  I54209
#authors   Rommens, J.M.; Durocher, F.; McArthur, J.; Tonin, P.;
           Leblanc, J.
#journal   Genomics (1995) 28:530-542
#title     Generation of a transcription map at the HSD17B locus
           centromeric to BRCA1 at 17q21.
#accession I68524
##status   preliminary; translated from GB/EMBL/DBDJ
##molecule_type  mRNA
##residues      1-117 ##label RES
##cross-references  GB:U38941; NID:g1008855; CDS_PID:g1008856
SUMMARY          #length 117 #molecular-weight 13305 #checksum 4392

Query Match      40.4%; Score 57; DB 13; Length 117;
Best Local Similarity 41.7%; Pred. No. 2.56e+00;
Matches          5; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Db 80 gsmcackcvrdri 91
   |::|::|::|::
QY 6 GTKSSKCVROKQV 17

##status      preliminary; translated from GB/EMBL/DBDJ
##molecule_type  mRNA
##residues      1-264 ##label ROM
##cross-references  EMBL:U34973; NID:g1063624; CDS_PID:g1063625
SUMMARY          #length 264 #molecular-weight 29057 #checksum 6729

Query Match      40.4%; Score 57; DB 16; Length 264;
Best Local Similarity 40.0%; Pred. No. 2.56e+00;
Matches          6; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Db 171 gataagcyrhveda 185
   |::|::|::|::|::
QY 6 GTRSSKCVROKVEGS 20

RESULT 9
ENTRY   B33485      #type complete
TITLE   spore coat protein SP70 - slime mold (Dictyostelium
           discoideum)
ORGANISM #formal_name Dictyostelium discoideum
DATE     09-Mar-1990 #sequence_revision 11-Sep-1992 #text_change
30-Sep-1993
ACCESSIONS B33485
REFERENCE  A33485
#authors   Fosnaugh, K.L.; Loomis, W.F.
#journal   Mol. Cell. Biol. (1989) 9:5215-5218
#title     Spore coat genes SP60 and SP70 of Dictyostelium discoideum.
#cross-references  MUID:90097939
#accession B33485
##status   preliminary
##molecule_type  DNA; mRNA
##residues      1-537 ##label FOS
##cross-references  GB:M26238
##note        the authors translated the codon AAT for residue 281 as
           Asp
CLASSIFICATION #superfamily LDL receptor ligand-binding repeat homology
SUMMARY          #length 537 #molecular-weight 56650 #checksum 2250

Query Match      39.7%; Score 56; DB 11; Length 537;
Best Local Similarity 54.5%; Pred. No. 3.89e+00;
Matches          6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Db 291 kngcirdkve 301
   |::|::|::|::
QY 8 KSSKCVROKVE 18

RESULT 10
ENTRY   S21825      #type complete
TITLE   vicillin-like storage protein g1b1-S, embryo - maize
ORGANISM #formal_name Zea mays #common_name maize
DATE     20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change
20-Feb-1995
ACCESSIONS S21825
REFERENCE  S21823
#authors   Kriz, A.L.
#submission submitted to the EMBL Data Library, April 1991
#accession S21825

```

```

##status      preliminary
##molecule_type DNA
##residues    1-540 #label KRI
##cross-references EMBL:X59084
GENETICS
#gene         Gbl1-S
#introns      170/1; 195/2; 222/2; 319/2
SUMMARY
#length 540 #molecular-weight 60239 #checksum 1419
Query Match      39.7%; Score 56; DB 11; Length 540;
Best Local Similarity 58.3%; Pred. No. 3.89e+00;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Db 32 hgghksgrcvrr 43
Qy 4 HQGTRKSKCVRRQ 15

RESULT 11
ENTRY
TITLE      A53234 #type complete
ORGANISM   globulin-1S, GLB1S - maize
DATE       02-May-1994 #sequence_revision 18-Nov-1994 #text_change
ACCESSIONS A53234
REFERENCE   A53234
#authors   Belanger, F.C.; Kriz, A.L.
#journal   Genetics (1991) 129:863-872
#title     Molecular basis for allelic polymorphism of the maize
#cross-references MUID:92090707
#accession A53234
##status   preliminary
##molecule_type DNA
##residues 1-573 #label BEL
##cross-references NCBI:71280; NCBI:P:71284
##experimental_source inbred line Va 26
##note     #length 573 #molecular-weight 65075 #checksum 3569
SUMMARY
Query Match      39.7%; Score 56; DB 11; Length 573;
Best Local Similarity 58.3%; Pred. No. 3.89e+00;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Db 32 hgghksgrcvrr 43
Qy 4 HQGTRKSKCVRRQ 15

RESULT 12
ENTRY
TITLE      A32494 #type complete
ORGANISM   transposable element Txc protein 1 - African clawed frog
DATE       12-Oct-1989 #sequence_revision 31-Dec-1993 #text_change
ACCESSIONS A32494
REFERENCE   A32494
#authors   Garrett, J.E.; Knutson, D.S.; Carroll, D.
#journal   Mol. Cell. Biol. (1989) 9:3018-3027
#title     Composite transposable elements in the Xenopus laevis genome.
#cross-references MUID:89384562
#accession A32494
##status   preliminary
##molecule_type DNA
##residues 1-775 #label GAR
##cross-references GB:M26915
##note     the authors translated the codon ATT for residue as Gln,
           and AAG for residue 288 as Leu
SUMMARY
#length 775 #molecular-weight 82355 #checksum 6734
Query Match      39.0%; Score 55; DB 13; Length 775;
Best Local Similarity 46.7%; Pred. No. 5.88e+00;
Matches 7; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

##status      preliminary
##molecule_type DNA
##residues    1-540 #label KRI
##cross-references EMBL:X59084
GENETICS
#gene         Gbl1-S
#introns      170/1; 195/2; 222/2; 319/2
SUMMARY
#length 540 #molecular-weight 60239 #checksum 1419
Query Match      39.7%; Score 56; DB 11; Length 540;
Best Local Similarity 58.3%; Pred. No. 3.89e+00;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Db 32 hgghksgrcvrr 43
Qy 4 HQGTRKSKCVRRQ 15

RESULT 11
ENTRY
TITLE      A53234 #type complete
ORGANISM   globulin-1S, GLB1S - maize
DATE       02-May-1994 #sequence_revision 18-Nov-1994 #text_change
ACCESSIONS A53234
REFERENCE   A53234
#authors   Belanger, F.C.; Kriz, A.L.
#journal   Genetics (1991) 129:863-872
#title     Molecular basis for allelic polymorphism of the maize
#cross-references MUID:92090707
#accession A53234
##status   preliminary
##molecule_type DNA
##residues 1-573 #label BEL
##cross-references NCBI:71280; NCBI:P:71284
##experimental_source inbred line Va 26
##note     #length 573 #molecular-weight 65075 #checksum 3569
SUMMARY
Query Match      39.7%; Score 56; DB 11; Length 573;
Best Local Similarity 58.3%; Pred. No. 3.89e+00;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Db 32 hgghksgrcvrr 43
Qy 4 HQGTRKSKCVRRQ 15

RESULT 12
ENTRY
TITLE      A32494 #type complete
ORGANISM   transposable element Txc protein 1 - African clawed frog
DATE       12-Oct-1989 #sequence_revision 31-Dec-1993 #text_change
ACCESSIONS A32494
REFERENCE   A32494
#authors   Garrett, J.E.; Knutson, D.S.; Carroll, D.
#journal   Mol. Cell. Biol. (1989) 9:3018-3027
#title     Composite transposable elements in the Xenopus laevis genome.
#cross-references MUID:89384562
#accession A32494
##status   preliminary
##molecule_type DNA
##residues 1-775 #label GAR
##cross-references GB:M26915
##note     the authors translated the codon ATT for residue as Gln,
           and AAG for residue 288 as Leu
SUMMARY
#length 775 #molecular-weight 82355 #checksum 6734
Query Match      39.0%; Score 55; DB 13; Length 775;
Best Local Similarity 46.7%; Pred. No. 5.88e+00;
Matches 7; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Db 617 sntskcvsevegtp 631
Qy 7 TKSSKCVRRQVEGSS 21

RESULT 13
ENTRY
TITLE      E47119 #type complete
ORGANISM   spore coat peptide CotZ - Bacillus subtilis
DATE       21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change
ACCESSIONS E47119
REFERENCE   E47119
#authors   Zhang, J.; Fitz-James, P.C.; Aronson, A.I.
#journal   J. Bacteriol. (1993) 175:3757-3766
#title     Cloning and characterization of a cluster of genes encoding
           polypeptides present in the insoluble fraction of the spore
           coat of Bacillus subtilis.
#cross-references MUID:93285989
#accession E47119
##status   preliminary
##molecule_type nucleic acid
##residues 1-148 #label ZHA
##cross-references NCBI:133538; NCBI:P:133548
##note     #length 148 #molecular-weight 16534 #checksum 4681
SUMMARY
Query Match      38.3%; Score 54; DB 10; Length 148;
Best Local Similarity 63.6%; Pred. No. 8.85e+00;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Db 4 ktsscvcveave 14
Qy 8 KSSKCVRRQKVE 18

RESULT 14
ENTRY
TITLE      G64383 #type complete
ORGANISM   riboflavin-specific deaminase (EC 3.5.4.-) - Methanococcus
DATE       13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change
ACCESSIONS G64383
REFERENCE   A64300
#authors   Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann,
           R.D.; Sutton, G.G.; Blake, J.A.; FitzGerald, L.M.; Clayton,
           R.A.; Gocayne, J.D.; Kerlavage, A.R.; Dougherty, B.A.;
           Tomb, J.F.; Adams, M.D.; Reich, C.I.; Overbeek, R.;
           Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.;
           Scott, J.L.; Geoghegan, N.S.M.; Weidman, J.F.; Fuhrmann,
           J.L.; Nguyen, D.; Usterback, T.R.; Kelley, J.M.; Peterson,
           J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts,
           K.M.; Hurst, M.A.; Kaine, B.P.; Borodovsky, M.; Klenk,
           H.P.; Fraser, C.M.; Smith, H.O.; Woese, C.R.; Venter, J.C.
           Science (1996) 273:1058-1073
#journal   Complete genome sequence of the methanogenic archaeon,
#title     Methanococcus jannaschii.
#accession G64383
##status   preliminary; nucleic acid sequence not shown;
           translation not shown
##molecule_type DNA
##residues 1-224 #label BUL
##cross-references GB:L77117; TIGR:MJ0671; CDS_PID:g1510756
GENETICS
#map_position REV597638-596964
#start_codon TTG
#keywords   hydrolase
SUMMARY
#length 224 #molecular-weight 25037 #checksum 2215
Query Match      38.3%; Score 54; DB 10; Length 224;
Best Local Similarity 33.3%; Pred. No. 8.85e+00;

```

Matches 6; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

Db 118 illdmgvkvkgrgkv 135
::: | | | | |
QY 1 VIDHQTKSKCVRQKVE 18

RESULT 15

ENTRY #type complete
TITLE P element - fruit fly (*Drosophila ananassae*)
ORGANISM #formal_name *Drosophila bifasciata*
DATE 01-Feb-1995 #sequence_revision 01-Feb-1995 #text_change

ACCESSIONS S46281
REFERENCE S46281
#authors Hagemann, S.; Miller, W.J.; Pinsker, W.
#journal Mol. Gen. Genet. (1994) 244:168-175
#title Two distinct P element subfamilies in the genome of *Drosophila bifasciata*.

#accession S46281
#status preliminary
#residues 1-562 #label HAG
SUMMARY #length 562 #molecular-weight 64682 #checksum 782

Query Match 38.3%; Score 54; DB 16; Length 562;
Best Local Similarity 41.2%; Pred. No. 8.85e+00;
Matches 7; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

Db 97 vinhtsmektlrqki 113
||: | | | | |
QY 1 VIDHQTKSKCVRQKV 17

RESULT 16

ENTRY #type complete
TITLE hypothetical protein YHR028c - yeast (*Saccharomyces cerevisiae*)
ORGANISM #formal_name *Saccharomyces cerevisiae*
DATE 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change

ACCESSIONS S46780
REFERENCE S46772
#authors Du, Z.
#submission submitted to the EMBL Data Library, June 1994
#description The sequence of *S. cerevisiae* cosmid 8082.
#accession S46780

#status preliminary
#molecule_type DNA
#residues 1-818 #label DUZ
#cross-references EMBL:U10399

GENETICS
#map_position 8R
CLASSIFICATION #superfamily dipeptidyl-peptidase IV
SUMMARY #length 818 #molecular-weight 93404 #checksum 2391

Query Match 38.3%; Score 54; DB 5; Length 818;
Best Local Similarity 33.3%; Pred. No. 8.85e+00;
Matches 7; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

Db 511 ivdfharkaeckdkgvlgks 531
::: | | | | |
QY 1 VIDHQTKSKCVRQKVESS 21

RESULT 17

ENTRY #type complete
TITLE dipeptidyl aminopeptidase B (EC 3.4.14.-) - yeast (*Saccharomyces cerevisiae*)
ORGANISM #formal_name *Saccharomyces cerevisiae*
DATE 07-Jun-1990 #sequence_revision 08-Mar-1996 #text_change

ACCESSIONS A30107
REFERENCE A30107

#authors Roberts, C.J.; Pohlig, G.; Rothman, J.H.; Stevens, T.H.
#journal J. Cell Biol. (1989) 108:1363-1373
#title Structure, biosynthesis, and localization of dipeptidyl aminopeptidase B, an integral membrane glycoprotein of the yeast vacuole.

#cross-references MUID:89174971
#accession A30107
#molecule_type DNA
#residues 1-841 #label ROB
#cross-references EMBL:X15484
#note the authors translated the codon ACC for residue 571 as Asn

GENETICS
#gene LISTA:DAP2; STE13
#map_position 15R
CLASSIFICATION #superfamily dipeptidyl-peptidase IV
KEYWORDS dipeptidylpeptidase hydrolase; glycoprotein; transmembrane protein
FEATURE 30-45 #domain transmembrane #status predicted #label TMV
63,79,110,139,391, #binding_site carbohydrate (Asn) (covalent) #status predicted
420
SUMMARY #length 841 #molecular-weight 96416 #checksum 1272

Query Match 38.3%; Score 54; DB 1; Length 841;
Best Local Similarity 33.3%; Pred. No. 8.85e+00;
Matches 7; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

Db 510 ivdfharkaeckdkgvlgks 530
::: | | | | |
QY 1 VIDHQTKSKCVRQKVESS 21

RESULT 18

ENTRY #type complete
TITLE probable membrane protein YOL089c - yeast (*Saccharomyces cerevisiae*)
ALTERNATE_NAMES hypothetical protein O0938
ORGANISM #formal_name *Saccharomyces cerevisiae*
DATE 28-Oct-1995 #sequence_revision 03-Nov-1995 #text_change

ACCESSIONS S57380; S66783; S50416
REFERENCE S57374
#authors Zumstein, E.; Pearson, B.M.; Kalogeropoulos, A.; Schweizer, M.

#journal Yeast (1995) 11:975-986
#title A 29.425 kb segment on the left arm of yeast chromosome XV contains more than twice as many unknown as known open reading frames.

#accession S57380
#status nucleic acid sequence not shown
#molecule_type DNA
#residues 1-1030 #label ZUM
#cross-references EMBL:X83121

REFERENCE S66775
#authors Zumstein, E.; Pearson, B.M.; Kalogeropoulos, A.; Schweizer, M.

#submission submitted to the Protein Sequence Database, July 1996
#accession S66783
#molecule_type DNA
#residues 1-1030 #label ZUM
#cross-references EMBL:Z74831
#experimental_source strain S288C

GENETICS
#map_position 15L
CLASSIFICATION #superfamily GAL4 zinc binuclear cluster homology
KEYWORDS transmembrane protein
FEATURE 131-171 #domain GAL4 zinc binuclear cluster homology #label GAL4
762-778 #domain transmembrane #status predicted #label TMV
SUMMARY #length 1030 #molecular-weight 117925 #checksum 6585

Query Match 38.3%; Score 54; DB 12; Length 1030;
 Best Local Similarity 38.5%; Pred. No. 8.85e+00;
 Matches 5; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Db 149 vdgqtkkscncik 161
 :||| |||:
 QY 2 IDHQGTRSKCVR 14

RESULT 19
 ENTRY Q4ADE5 #type complete
 TITLE early E4 11K protein - human adenovirus 5
 ORGANISM #formal_name Mastadenovirus h5 #common_name human adenovirus 5
 #note host Homo sapiens (man)
 DATE 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change
 ACCESSIONS B03807; A03807
 REFERENCE A92890
 #authors Sarnow, P.; Hearing, P.; Anderson, C.W.; Reich, N.; Levine, A.J.
 #journal J. Mol. Biol. (1982) 162:565-583
 #title Identification and characterization of an immunologically conserved adenovirus early region 11,000 M-r protein and its association with the nuclear matrix.
 #cross-references MUID:83164198
 #accession B03807
 #molecule_type DNA
 #residues 1-116 #label SAR
 GENETICS
 #map_position 96.0-97.0
 CLASSIFICATION #superfamily adenovirus early E4 11K protein
 KEYWORDS early protein
 SUMMARY #length 116 #molecular-weight 13298 #checksum 6308

Query Match 37.6%; Score 53; DB 4; Length 116;
 Best Local Similarity 60.0%; Pred. No. 1.33e+01;
 Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Db 3 rclrlkvega 12
 :||| |||:
 QY 11 KCVQKVEGS 20

RESULT 20
 ENTRY Q4ADE2 #type complete
 TITLE early E4 11K protein - human adenovirus 2
 ORGANISM #formal_name Mastadenovirus h2 #common_name human adenovirus 2
 #note host Homo sapiens (man)
 DATE 02-Apr-1982 #sequence_revision 02-Apr-1982 #text_change
 ACCESSIONS A03807
 REFERENCE A93733
 #authors Herisse, J.; Rigolet, M.; Dupont de Dinechin, S.; Galibert, F.
 #journal Nucleic Acids Res. (1981) 9:4023-4042
 #title Nucleotide sequence of adenovirus 2 DNA fragment encoding for the carboxylic region of the fiber protein and the entire E4 region.
 #cross-references MUID:82059444
 #accession A03807
 #molecule_type DNA
 #residues 1-116 #label HER
 #note this protein was assigned by correlating EM data and S1 digestion studies
 GENETICS
 #map_position 96.0-97.0
 CLASSIFICATION #superfamily adenovirus early E4 11K protein
 KEYWORDS early protein
 SUMMARY #length 116 #molecular-weight 13255 #checksum 6011

Query Match 37.6%; Score 53; DB 4; Length 116;
 Best Local Similarity 60.0%; Pred. No. 1.33e+01;
 Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Db 3 rclrlkvega 12
 :||| |||:
 QY 11 KCVQKVEGS 20

RESULT 21
 ENTRY S41772 #type complete
 TITLE glycine-rich RNA-binding protein RGP-1b - wood tobacco
 ORGANISM #formal_name Nicotiana sylvestris #common_name wood tobacco
 DATE 25-Dec-1994 #sequence_revision 01-Dec-1995 #text_change
 01-Dec-1995
 ACCESSIONS S41772
 REFERENCE Hirose, T.; Sugita, M.; Sugliura, M.
 #authors Nucleic Acids Res. (1993) 21:3981-3987
 #journal CDNA structure, expression and nucleic acid-binding
 #title properties of three RNA-binding proteins in tobacco: occurrence of tissue-specific alternative splicing.
 #accession S41772
 #molecule_type mRNA
 #residues 1-148 #label HIR
 #cross-references EMBL:D16205
 CLASSIFICATION #superfamily ribonucleoprotein repeat homology
 KEYWORDS RNA binding
 FEATURE 7-74
 SUMMARY #domain ribonucleoprotein repeat homology #label RRM1
 #length 148 #molecular-weight 14655 #checksum 1944

Query Match 37.6%; Score 53; DB 7; Length 148;
 Best Local Similarity 50.0%; Pred. No. 1.33e+01;
 Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Db 55 kdekcmrdaieg 66
 | ||| :||
 QY 8 KSSKCVQKVEG 19

RESULT 22
 ENTRY C38128 #type complete
 TITLE epithelin/granulin precursor - mouse
 ALTERNATE_NAMES acrogranin
 ORGANISM #formal_name Mus musculus #common_name house mouse
 DATE 10-Jul-1992 #sequence_revision 10-Jul-1992 #text_change
 15-Oct-1996
 ACCESSIONS C38128; S32503; I49468
 REFERENCE A38128
 #authors Plowman, G.D.; Green, J.M.; Neubauer, M.G.; Buckley, S.D.; McDonald, V.L.; Todaro, G.J.; Shoyab, M.
 #journal J. Biol. Chem. (1992) 267:13073-13078
 #title The epithelin precursor encodes two proteins with opposing activities on epithelial cell growth.
 #cross-references MUID:92317004
 #accession C38128
 #molecule_type mRNA
 #residues 1-589 #label PLO
 #cross-references GB:X62321
 REFERENCE S32503
 #authors Baba, T.; Nemoto, H.; Watanabe, K.; Arai, Y.; Gerton, G.L.
 #journal FEBS Lett. (1993) 322:89-94
 #title Exon/intron organization of the gene encoding the mouse epithelin/granulin precursor (acrogranin).
 #accession S32503
 #molecule_type DNA
 #residues 18-349, 'L', 351-589 #label BAB
 REFERENCE I48141
 #authors Baba, T.; Hoff, H.B.
 #journal Mol. Reprod. Dev. (1993) 34:233-243
 #title Acrogranin, an acrosomal cysteine-rich glycoprotein, is the precursor of the growth-modulating peptides, granulins, and

```

epithelins, and is expressed in somatic as well as male
germ cells.
#cross-references MUID:93228994
#accession 149468
#status preliminary; translated from GB/EMBL/DBJ
#molecule_type mRNA
#residues 1-250, 'L', 252-253, 'V', 255-349, 'L', 351-401, 'SA', 404-589
#label RES
#cross-references GB:M86736; NID:g191766; CDS_PID:g191767
CLASSIFICATION superfamily granulin
SUMMARY length 589 #molecular-weight 63501 #checksum 6927

Query Match 37.6%; Score 53; DB 7; Length 589;
Best Local Similarity 35.7%; Pred. No. 1.33e+01;
Matches 5; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

Db 560 hcsargtkclrkki 573
| : : : : | : | :
| : : : : | : | :
QY 4 HQGTSKSKVRQKV 17

RESULT 23
ENTRY S43428 #type complete
TITLE omega-crystallin - giant octopus
ORGANISM #formal_name Octopus dofleini #common_name giant octopus
DATE 07-Sep-1994 #sequence_revision 26-May-1995 #text_change
26-May-1995
ACCESSIONS S43428
REFERENCE S43425
#authors Tomarev, S.I.; Zinovleva, R.D.; Piatigorsky, J.
#journal Biochim. Biophys. Acta (1993) 1216:245-254
#title Primary structure and lens-specific expression of genes for
an intermediate filament protein and a beta-tubulin in
cephalopods.
#accession S43428
#status preliminary
#molecule_type mRNA
#residues 1-591 #label TOM
#cross-references EMBL:L10113
#note the authors did not translate the codon for residue 1
SUMMARY length 591 #molecular-weight 67287 #checksum 7420

Query Match 37.6%; Score 53; DB 12; Length 591;
Best Local Similarity 40.0%; Pred. No. 1.33e+01;
Matches 6; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

Db 51 ishkgvtdircnrek 65
| : : : : | : | :
| : : : : | : | :
QY 2 IDHQGTSKSKVRQK 16

RESULT 24
ENTRY I54205 #type complete
TITLE galactosylceramidase (EC 3.2.1.46) - human
ALTERNATE_NAMES galactocerebrosidase; galcerase
ORGANISM #formal_name Homo sapiens #common_name man
DATE 24-May-1996 #sequence_revision 24-May-1996 #text_change
04-Oct-1996
ACCESSIONS I54205; JC2397; PC2247; I54345
REFERENCE I54205
#authors Luzzi, P.; Rafi, M.A.; Wenger, D.A.
#journal Genomics (1995) 26:407-409
#title Structure and organization of the human galactocerebrosidase
(GALC) gene.
#cross-references MUID:95324938
#accession I54205
#status preliminary; translated from GB/EMBL/DBJ
#molecule_type DNA
#residues 1-669 #label RES
#cross-references GB:L38559; NID:g710533; CDS_PID:g710535
JC2397
#authors Sakai, N.; Inui, K.; Fujii, N.; Fukushima, H.; Nishimoto, J.;
Yanagihara, I.; Isegawa, Y.; Iwamatsu, A.; Okada, S.

```

```

#journal Biochem. Biophys. Res. Commun. (1994) 198:485-491
#title Krabbe disease: isolation and characterization of a
full-length cDNA for human galactocerebrosidase.
#accession JC2397
#molecule_type mRNA
#residues 1-545, 'I', 547-669 #label SAK
#accession PC2247
#molecule_type protein
#residues 229-245; 328-337; 343-350; 416-424; 436-447; 467-475; 632-643;
661-669 #label SA2
#cross-references DDBJ:D25283
REFERENCE I54345
#authors Chen, Y.O.; Rafi, M.A.; de Gala, G.; Wenger, D.A.
#journal Hum. Mol. Genet. (1993) 2:1841-1845
#title Cloning and expression of cDNA encoding human
galactocerebrosidase, the enzyme deficient in globoid cell
leukodystrophy.
#cross-references MUID:94108435
#accession I54345
#status preliminary; translated from GB/EMBL/DBJ
#molecule_type mRNA
#residues 1-545, 'I', 547-669 #label RE2
#cross-references GB:t23116; NID:g431309; CDS_PID:g431310
COMMENT This enzyme hydrolyzes the galactose ester bonds of
galactosylceramide, galactosylsphingosine,
monogalactosyldiglyceride and lactosylceramide.
GENETICS
#gene GDB:GALC
#cross-references GDB:I19970
#map_position 14q31-14q31
#introns 49/3; 72/3; 94/1; 132/1; 178/3; 191/3; 235/2; 287/2; 329/1;
371/3; 401/3; 430/3; 481/1; 541/2; 596/1; 621/3
KEYWORDS glycoprotein; glycosidase; hydrolase
FEATURE
1-26
27-669
127,363,387,540,
543,586
SUMMARY length 669 #molecular-weight 75135 #checksum 818

Query Match 37.6%; Score 53; DB 13; Length 669;
Best Local Similarity 42.9%; Pred. No. 1.33e+01;
Matches 6; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Db 367 iietmshkshkclir 380
| : : : : | : | :
| : : : : | : | :
QY 1 VIDHQGTSKSKVR 14

RESULT 25
ENTRY PFHUGA #type complete
TITLE platelet-derived growth factor receptor alpha precursor -
human
CONTAINS protein-tyrosine kinase (EC 2.7.1.112)
ORGANISM #formal_name Homo sapiens #common_name man
DATE 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change
13-Sep-1996
ACCESSIONS A40162; A32941
REFERENCE A40162
#authors Matsui, T.; Heidaran, M.; Miki, T.; Popescu, N.; La Rochelle,
W.; Kraus, M.; Pierce, J.; Aaronson, S.
#journal Science (1989) 243:800-804
#title Isolation of a novel receptor cDNA establishes the existence
of two PDGF receptor genes.
#cross-references MUID:89130149
#accession A40162
#molecule_type mRNA
#residues 1-1089 #label MATS
#cross-references GB:M21574
A32941
REFERENCE A32941
#authors Claesson-Welsh, L.; Eriksson, A.; Westermark, B.; Heldin,

```

```

C.H.
#journal Proc. Natl. Acad. Sci. U.S.A. (1989) 86:4917-4921
#title  CDNA cloning and expression of the human A-type
        platelet-derived growth factor (PDGF) receptor establishes
        structural similarity to the B-type PDGF receptor.
#cross-references MUID:89296915
#accession  A32941
#molecule_type mRNA
#residues 1-1089 #label CLA
#cross-references GB:M22734
COMMENT The extracellular domain is predicted to include five
        immunoglobulin-like domains.
GENETICS
#gene GDB:PDGFRA
#cross-references GDB:120267
#map_position 4q11-q12
CLASSIFICATION #superfamily macrophage colony-stimulating factor 1 receptor;
        immunoglobulin homology; protein kinase homology
KEYWORDS ATP; autophosphorylation; dimer; glycoprotein;
        phosphoprotein; phosphotransferase; transmembrane protein;
        tyrosine-specific protein kinase
FEATURE
1-24 #domain signal sequence #status predicted #label SIG\
25-1089 #product platelet-derived growth factor receptor alpha
        #status predicted #label MAT\
        #domain extracellular #status predicted #label EXT\
        #domain immunoglobulin homology #label IMM1\
        #domain immunoglobulin homology #label IMM2\
        #domain immunoglobulin homology #label IMM3\
        #domain immunoglobulin homology #label IMM4\
        #domain transmembrane #status predicted #label TMM\
        #domain intracellular #status predicted #label INT\
        #domain protein kinase homology #label KIN\
        #region protein kinase ATP-binding motif\
        #binding_site carbohydrate (Asn) (covalent) #status
        predicted\
        49-100,150-189,
        235-290,435-501 #disulfide_bonds #status predicted\
        627 #active_site Lys #status predicted\
        849 #binding_site phosphate (Tyr) (covalent) (by
        autophosphorylation) #status predicted
SUMMARY #length 1089 #molecular_weight 122668 #checksum 4547
Query Match 37.6%; Score 53; DB 1; Length 1089;
Best Local Similarity 38.1%; Pred. No. 1.33e+01;
Matches 8; Conservative 6; Mismatches 7; Indels 0; Gaps 0;
Db 421 vddhgstggtvrcraegtp 441
| | | : : : | | | :
Qy 1 VIDHQGTSSKCVQRKVEGSS 21

```

Search completed: Tue Jul 29 07:32:10 1997
Job time : 36 secs.

 W P I S R E F L

 (TM)

Release 2.1D John F. Collins, Biocomputing Research Unit.
 Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K.
 Distribution rights by IntelliGenetics, Inc.

MPSrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Tue Jul 29 07:30:59 1997; Maspar time 2.33 Seconds
 Tabular output not generated. 190.965 Million cell updates/sec

Title: >US-08-487-283A-1
 Description: (1-21) from US08487283A.pep
 Perfect Score: 141
 Sequence: 1 VIDHOGTKSKCVRKVEGSS 21

Scoring table:
 PAM 150
 Gap 15

Searched: 59021 seqs, 21210388 residues

Post-processing: Minimum Match 0%
 Listing first 100 summaries

Database: swiss-prot34
 1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
 8:part8 9:part9 10:part10 11:part11

Statistics: Mean 26.425; Variance 29.915; scale 0.883

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description	Pred. No.
1	141	100.0	1676	2	CO5_HUMAN	1.16e-24
2	69	48.9	1680	2	CO5_MOUSE	7.22e-04
3	59	41.8	943	5	IRQA_NEIME	1.65e-01
4	59	41.8	1002	11	YEMA_DROME	1.65e-01
5	57	40.4	116	8	RL34_HUMAN	60S RIBOSOMAL PROTEIN
6	57	40.4	264	2	CSH_ARTSP	N-CARBAMOYLSCAROSINE
7	56	39.7	537	9	SP70_DICDI	SPORE COAT PROTEIN SP
8	56	39.7	573	4	GLB1_MAIZE	GLOBULIN-1 S ALLELE P
9	56	39.7	1357	8	RPOB_PSEPU	DNA-DIRECTED RNA POLY
10	55	39.0	775	11	YTXL_XENLA	TRANSPONON TXI HYPOTH
11	54	38.3	148	2	COT2_BACSU	SPORE COAT PROTEIN 2
12	54	38.3	818	3	DAP2_YEAST	DIPEPTIDYL AMINOPEPTI
13	54	38.3	1039	11	YR71_CAEEL	HYPOTHETICAL 118.2 KD
14	53	37.6	116	3	E411_ADE05	PROBABLE EARLY E4 11
15	53	37.6	116	3	E411_ADE02	PROBABLE EARLY E4 11
16	53	37.6	589	4	GRN_MOUSE	GRANULINS PRECURSOR (
17	53	37.6	669	4	GALC_HUMAN	GALACTOCEREBROSIDASE
18	53	37.6	1089	7	PGDS_HUMAN	ALPHA PLATELET-DERIVE
19	52	36.9	329	3	ESG2_TRYBB	VSG EXPRESSION SITE-A
20	52	36.9	354	7	CDX2_AGR75	ORNITHINE CYCLODAMIN
21	52	36.9	455	7	P2X5_RAT	P2X PURINOCEPTOR 5 (A
22	51	36.2	121	11	YIF2_YEAST	PROBABLE 60S RIBOSOMA

23	51	36.2	337	10	VP67_NPVGM	MAJOR ENVELOPE GLYCOP	8.32e+00
24	51	36.2	337	1	ADH1_ZYMMO	ALCOHOL DEHYDROGENASE	8.32e+00
25	51	36.2	462	5	KPV1_ECOLI	PYRUVATE KINASE I (EC	8.32e+00
26	51	36.2	512	10	VP67_NPVAC	MAJOR ENVELOPE GLYCOP	8.32e+00
27	51	36.2	574	3	ESTR_SALIR	ESTROGEN RECEPTOR (ER	8.32e+00
28	51	36.2	588	4	GRN_RAT	GRANULINS PRECURSOR (8.32e+00
29	51	36.2	1056	6	MUC5_HUMAN	TRACHEOBRONCHIAL MUCI	8.32e+00
30	51	36.2	1651	10	VIT6_CAEEL	VITELLOGENIN 6 PRECUR	8.32e+00
31	51	36.2	1678	2	CLH_DROME	CLATHRIN HEAVY CHAIN	8.32e+00
32	50	35.5	123	8	RL14_HAEIN	50S RIBOSOMAL PROTEIN	1.32e+01
33	50	35.5	171	11	YJB6_YEAST	HYPOTHETICAL 19.7 KD	1.32e+01
34	50	35.5	192	10	Y045_NPVAC	HYPOTHETICAL 22.7 KD	1.32e+01
35	50	35.5	296	8	RBSB_ECOLI	D-RIBOSE-BINDING PERI	1.32e+01
36	50	35.5	296	8	RBSB_SALTY	D-RIBOSE-BINDING PERI	1.32e+01
37	50	35.5	301	9	TRF2_CHICK	TROPONIN T, CARDIAC M	1.32e+01
38	50	35.5	410	1	BEDA_PSEPU	BENZENE 1,2-DIOXYGENA	1.32e+01
39	50	35.5	592	5	INVA_DAUCA	BETA-FRUCTOFURANOSIDA	1.32e+01
40	50	35.5	1010	10	WNT5_DROME	PROTEIN DWNT-5 PRECUR	1.32e+01
41	49	34.8	72	10	VSM0_TRYBB	VARIANT SURFACE GLYC	2.06e+01
42	49	34.8	99	5	IT12_SIGNAL	TRYPSIN INHIBITOR 2 P	2.06e+01
43	49	34.8	121	8	RK14_OOSI	CHLOROPLAST 50S RIBOS	2.06e+01
44	49	34.8	122	8	RL14_PORPU	CHLOROPLAST 50S RIBOS	2.06e+01
45	49	34.8	122	8	RL14_THETH	50S RIBOSOMAL PROTEIN	2.06e+01
46	49	34.8	175	10	Y04G_MYCTU	HYPOTHETICAL 19.3 KD	2.06e+01
47	49	34.8	220	1	ANTA_HYDMA	ANTISTATIN PRECURSOR	2.06e+01
48	49	34.8	222	8	PSPA_ECOLI	PHAGE SHOCK PROTEIN A	2.06e+01
49	49	34.8	267	11	YD6A_SCHPO	HYPOTHETICAL 30.6 KD	2.06e+01
50	49	34.8	424	11	ZFP1_MOUSE	ZINC FINGER PROTEIN 2	2.06e+01
51	49	34.8	429	6	NCAP_HANTV	NUCLEOCAPSID PROTEIN	2.06e+01
52	49	34.8	487	5	HR3_DROME	PROBABLE NUCLEAR HORM	2.06e+01
53	49	34.8	509	10	VP67_NPVCF	MAJOR ENVELOPE GLYCOP	2.06e+01
54	49	34.8	591	4	FUCI_ECOLI	L-FUCOSE ISOMERASE (E	2.06e+01
55	49	34.8	660	2	CIR4_BOVIN	POTASSIUM CHANNEL PRO	2.06e+01
56	49	34.8	732	9	TRI6_ECOLI	TRAI PROTEIN	2.06e+01
57	49	34.8	752	6	NSF2_DROME	VESICULAR-FUSION PROT	2.06e+01
58	49	34.8	784	4	GCF_HUMAN	GC-RICH SEQUENCE DNA-	2.06e+01
59	49	34.8	1088	7	PGDS_RAT	ALPHA PLATELET-DERIVE	2.06e+01
60	49	34.8	1323	6	NME4_MOUSE	GLUTAMATE (NMDA) RECE	2.06e+01
61	49	34.8	1451	1	A2MH_MOUSE	MURINOGLOBULIN 2 PREC	2.06e+01
62	49	34.8	1476	1	A2MG_MOUSE	MURINOGLOBULIN 1 PREC	2.06e+01
63	48	34.0	233	8	RL1_ECOLI	50S RIBOSOMAL PROTEIN	3.21e+01
64	48	34.0	339	9	TF3A_BUFAM	TRANSCRIPTION FACTOR	3.21e+01
65	48	34.0	353	6	NOV_COTJA	NOV PROTEIN PRECURSOR	3.21e+01
66	48	34.0	376	3	DUT_HSV62	DEOXYURIDINE 5'-TRIPH	3.21e+01
67	48	34.0	399	7	P2X1_HUMAN	P2X PURINOCEPTOR 1 (A	3.21e+01
68	48	34.0	481	3	DPOL_HPBVV	DNA POLYMERASE (EC 2	3.21e+01
69	48	34.0	683	9	SEF1_YEAST	ZINC FINGER PROTEIN S	3.21e+01
70	48	34.0	791	5	KDGG_HUMAN	DIACYLGLYCEROL KINASE	3.21e+01
71	48	34.0	845	3	DPOL_HPBV2	DNA POLYMERASE (EC 2	3.21e+01
72	48	34.0	873	7	PC1_HUMAN	PLASMA-CELL MEMBRANE	3.21e+01
73	48	34.0	953	11	YNM7_YEAST	HYPOTHETICAL 109.8 KD	3.21e+01
74	48	34.0	974	1	ATXB_LEIDO	PROBABLE E1-E2 TYPE C	3.21e+01
75	48	34.0	974	1	ATXA_LEIDO	PROBABLE E1-E2 TYPE C	3.21e+01
76	48	34.0	1216	1	ATC2_YEAST	PROBABLE CALCIUM-TRAN	3.21e+01
77	48	34.0	1296	1	ASAI_ENTFA	AGGREGATION SUBSTANCE	3.21e+01
78	48	34.0	1350	10	VG72_HSV11	HYPOTHETICAL GENE 72	3.21e+01
79	47	33.3	47	8	RK14_VIGUN	CHLOROPLAST 50S RIBOS	4.95e+01
80	47	33.3	100	11	YHBQ_ECOLI	HYPOTHETICAL 11.3 KD	4.95e+01
81	47	33.3	122	8	RK14_CHLRE	CHLOROPLAST 50S RIBOS	4.95e+01
82	47	33.3	123	8	RK14_TOBAC	CHLOROPLAST 50S RIBOS	4.95e+01
83	47	33.3	157	8	RS7_CHUTR	30S RIBOSOMAL PROTEIN	4.95e+01
84	47	33.3	179	11	YPU1_BACSU	HYPOTHETICAL 20.4 KD	4.95e+01
85	47	33.3	277	5	NOB_PLAFD	NOB-ASSOCIATED HISTI	4.95e+01
86	47	33.3	343	6	NOV_XENLA	NOV PROTEIN HOMOLOG P	4.95e+01
87	47	33.3	348	11	YLM1_CAEEL	HYPOTHETICAL 41.0 KD	4.95e+01
88	47	33.3	394	3	EFTU_BORBU	ELONGATION FACTOR TU	4.95e+01
89	47	33.3	473	5	NOB_PLAFA	NOB-ASSOCIATED HISTI	4.95e+01
90	47	33.3	491	2	CPI1_CHICK	CYTOCHROME P450 ITH1	4.95e+01
91	47	33.3	498	4	GAG_HV10Y	GAG POLYPROTEIN (CONT	4.95e+01
92	47	33.3	499	4	GAG_HV1Y2	GAG POLYPROTEIN (CONT	4.95e+01
93	47	33.3	634	5	NOB_PLAFA	NOB-ASSOCIATED HISTI	4.95e+01
94	47	33.3	634	5	NOB_PLAFA	NOB-ASSOCIATED HISTI	4.95e+01
95	47	33.3	727	7	NUAN_BOVIN	NADH-UBIQUINONE OXIDO	4.95e+01

96 47 33.3 727 7 NUAM_HUMAN NADH-UBIQUINONE OXIDO 4.95e+01
 97 47 33.3 763 3 DPOL_HPEVP DNA POLYMERASE (EC 2. 4.95e+01
 98 47 33.3 1080 3 CYA7_HUMAN ADENYLATE CYCLASE, TY 4.95e+01
 99 47 33.3 1099 3 CYA7_MOUSE ADENYLATE CYCLASE, TY 4.95e+01
 100 47 33.3 1500 1 AT7A_HUMAN COPPER-TRANSPORTING A 4.95e+01

ALIGNMENTS

```

RESULT 1
ID CO5_HUMAN STANDARD; PRT; 1676 AA.
AC P01031;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 01-DEC-1992 (REL. 24, LAST SEQUENCE UPDATE)
DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
DE COMPLEMENT C5 PRECURSOR (CONTAINS: C5A ANAPHYLATOXIN).
GN C5.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
[1]
RN SIGNAL; POLYMORPHISM.
RP SEQUENCE FROM N.A.
RX MEDLINE; 91079575.
RA HAVILAND D.L., HAVILAND J.C., FLEISCHER D.T., HUNT A., WETSEL R.A.;
RL J. IMMUNOL. 146:362-368(1991).
[2]
RN SEQUENCE OF 412-1676 FROM N.A.
RX MEDLINE; 88209511.
RA WETSEL R.A., LEMONS R.S., LEBEAU M.M., BARNUM S.R., NOACK D.,
RA TACK B.F.;
RL BIOCHEMISTRY 27:1474-1482(1988).
[3]
RN SEQUENCE OF 412-902 FROM N.A.
RX MEDLINE; 85130937.
RA LUNDWALL A.B., WETSEL R.A., KRISTENSEN T., WHITEHEAD A.S.,
RA WOODS D.E., OGDEN R.C., COITEN H.R., TACK B.F.;
RL J. BIOL. CHEM. 260:2108-2112(1985).
[4]
RN SEQUENCE OF 678-751.
RX MEDLINE; 79005687.
RA FERNANDEZ H.N., HUGLI T.E.;
RL J. BIOL. CHEM. 253:6955-6964(1978).
[5]
RN SEQUENCE OF 678-751 FROM N.A.
RX MEDLINE; 91144547.
RA BOHSACK J.F., MOLLISON K.W., BUKO A.M., ASHWORTH J.C., HILL H.R.;
RL BIOCHEM. J. 273:635-640(1991).
[6]
RN STRUCTURE BY NMR OF C5A.
RX MEDLINE; 88309754.
RA ZUIDERWEG E.R., MOLLISON K.W., HENKIN J., CARTER G.W.;
RL BIOCHEMISTRY 27:3568-3580(1988).
[7]
RN STRUCTURE BY NMR OF C5A.
RX MEDLINE; 89207527.
RA ZUIDERWEG E.R., NETTESHEIM D.G., MOLLISON K.W., CARTER G.W.;
RL BIOCHEMISTRY 28:172-185(1989).
[8]
RN STRUCTURE BY NMR OF C5A.
RX MEDLINE; 89274164.
RA ZUIDERWEG E.R., PESIK S.W.;
RL BIOCHEMISTRY 28:2387-2391(1989).
CC -!- FUNCTION: ACTIVATION OF C5 BY A C5 CONVERTASE INITIATES THE
CC SPONTANEOUS ASSEMBLY OF THE LATE COMPLEMENT COMPONENTS, C5-C9,
CC INTO THE MEMBRANE ATTACK COMPLEX. C5B HAS A TRANSIENT BINDING SITE
CC FOR C6. THE C5B-C6 COMPLEX IS THE FOUNDATION UPON WHICH THE LYCIC
CC COMPLEX IS ASSEMBLED.
CC -!- SUBUNIT: C5 PRECURSOR IS FIRST PROCESSED BY THE REMOVAL OF 4 BASIC
CC RESIDUES, FORMING TWO CHAINS, BETA & ALPHA, LINKED BY A DISULFIDE
CC BOND. C5 CONVERTASE ACTIVATES C5 BY CLEAVING THE ALPHA CHAIN,
CC RELEASING C5A ANAPHYLATOXIN & GENERATING C5B (BETA CHAIN + ALPHA'
CC CHAIN).
CC -!- SIMILARITY: TO C3, C4 AND ALPHA-2-MACROGLOBULIN.

```

```

CC -!- FUNCTION: DERIVED FROM PROTEOLYTIC DEGRADATION OF COMPLEMENT C5,
CC C5 ANAPHYLATOXIN IS A MEDIATOR OF LOCAL INFLAMMATORY PROCESS. IT
CC INDICES THE CONTRACTION OF SMOOTH MUSCLE, INCREASES VASCULAR
CC PERMEABILITY AND CAUSES HISTAMINE RELEASE FROM MAST CELLS AND
CC BASOPHILIC LEUKOCYTES. C5A ALSO STIMULATES THE LOCOMOTION OF
CC POLYMPHONUCLEAR LEUKOCYTES (CHEMOKINESIS) AND DIRECT THEIR
CC MIGRATION TOWARD SITES OF INFLAMMATION (CHEMOTAXIS).
CC -!- CAUTION: REF.3 SEQUENCE DIFFERS FROM THAT SHOWN FROM POSITION 855
CC ONWARD DUE TO THE PRESENCE OF AN ALU REPEAT.
CC -!- SIMILARITY: CONTAINS ONE ANAPHYLATOXIN-LIKE DOMAIN.
DR EMBL; M57729; G179983; -.
DR EMBL; M65134; G179692; -.
DR PIR; A40075; C5HU.
DR PIR; S15121; S15121.
DR HSSP; P01032; 1C5A.
DR MIM; 120900; -.
DR PROSITE; PS00477; ALPHA_2_MACROGLOBULIN.
KW COMPLEMENT PATHWAY; COMPLEMENT ALTERNATE PATHWAY; GLYCOPROTEIN;
KW PLASMA; MEMBRANE ATTACK COMPLEX; CYTOLYSIS; INFLAMMATORY RESPONSE;
KW SIGNAL; POLYMORPHISM.
FT SIGNAL 1 18 POTENTIAL.
FT CHAIN 19 673 COMPLEMENT C5 BETA CHAIN.
FT PROPEP 674 677
FT CHAIN 678 1676 COMPLEMENT C5 ALPHA CHAIN.
FT PEPTIDE 678 751 C5A ANAPHYLATOXIN.
FT CHAIN 752 1676 C5B (ALPHA').
FT DOMAIN 698 732 ANAPHYLATOXIN-LIKE.
FT DISULFID 698 724
FT DISULFID 699 731
FT DISULFID 711 732
FT CARBOHYD 741 741
FT CARBOHYD 911 911 POTENTIAL.
FT CARBOHYD 1115 1115 POTENTIAL.
FT CARBOHYD 1630 1630 POTENTIAL.
FT VARIANT 518 518 F -> S.
SQ SEQUENCE 1676 AA; 188331 MW; 9D5C6E59 CRC32;
Query Match 100.0%; Score 141; DB 2; Length 1676;
Best Local Similarity 100.0%; Pred. No. 1.16e-24;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 872 vidhgtksskcvrkqvegss 892
| | | | | | | | | | | | | | | | | | | | | |
QY 1 VIDHGTKSSKCVRKQVEGSS 21
| | | | | | | | | | | | | | | | | | | | | |
RESULT 2
ID CO5_MOUSE STANDARD; PRT; 1680 AA.
AC P06584;
DT 01-JAN-1988 (REL. 06, CREATED)
DT 01-NOV-1990 (REL. 16, LAST SEQUENCE UPDATE)
DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
DE COMPLEMENT C5 PRECURSOR (CONTAINS: C5A ANAPHYLATOXIN).
GN C5.
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 90153853.
RA WETSEL R.A., FLEISCHER D.T., HAVILAND D.L.;
RL J. BIOL. CHEM. 265:2435-2440(1990).
[2]
RN SEQUENCE OF 41-1680 FROM N.A.
RX MEDLINE; 87185363.
RA WETSEL R.A., OGATA R.T., TACK B.F.;
RL BIOCHEMISTRY 26:737-743(1987).
CC -!- FUNCTION: ACTIVATION OF C5 BY A C5 CONVERTASE INITIATES THE
CC SPONTANEOUS ASSEMBLY OF THE LATE COMPLEMENT COMPONENTS, C5-C9,
CC INTO THE MEMBRANE ATTACK COMPLEX. C5B HAS A TRANSIENT BINDING SITE
CC FOR C6. THE C5B-C6 COMPLEX IS THE FOUNDATION UPON WHICH THE LYCIC
CC COMPLEX IS ASSEMBLED.
CC -!- SUBUNIT: C5 PRECURSOR IS FIRST PROCESSED BY THE REMOVAL OF 4 BASIC

```



```

RC TISSUE-OVARY;
RX MEDLINE; 96039267.
RA ROMMENS J.M., DUROCHER F., MCARTHUR J., TONIN P., LEBLANC J.F.,
RL ALLEN T., SAMSON C., FERRI L., NAROD S., MORGAN K., SIMARD J.;
RL GENOMICS 28:530-542(1995).
CC -1- SIMILARITY: BELONGS TO THE L34E FAMILY OF RIBOSOMAL PROTEINS.
DR EMBL; L38941; G1008856; -.
KW RIBOSOMAL PROTEIN.
FT INIT_MET 0
SQ SEQUENCE 116 AA; 13174 MW; 490F4AF1 CRC32;

Query Match 40.4%; Score 57; DB 8; Length 116;
Best Local Similarity 41.7%; Pred. No. 4.57e-01;
Matches 5; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Db 79 gsmcakcvrdri 90
QY 5 GTKSKCVQKV 17
I:::|||||:::

RESULT 6
ID CSH ARTSP STANDARD; PRT; 264 AA.
AC P32400;
DT 01-OCT-1993 (REL. 27, CREATED)
DT 01-OCT-1993 (REL. 27, LAST SEQUENCE UPDATE)
DT 01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)
DE N-CARBAMOYLARCOSINE AMIDASE (EC 3.5.1.59) (N-CARBAMOYLARCOSINE
DE AMIDOHYDROLASE) (CSHASE).
OS ARTHROBACTER SP.
OC PROKARYOTA; FIRMICUTES; IRREGULAR ASPOROGENOUS RODS; CORYNEFORM GROUP.
RN [1]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS), AND REVISIONS TO 184 AND 232.
RX MEDLINE; 92389321.
RA ROMAO M.J., TURK D., GOMIS-RUETH F.-X., HUBER R.;
RL J. MOL. BIOL. 226:1111-1130(1992).
CC -1- CATALYTIC ACTIVITY: N-CARBAMOYLARCOSINE + H(2)O - SARCOSE +
CC CO(2) + NH(3).
CC -1- SUBUNIT: HOMOTETRAMER.
CC -1- COFACTOR: ONE SULFATE ION PER SUBUNIT.
CC -1- PATHWAY: DEGRADATION OF CREATININE TO GLYCINE.
DR PIR; S28969; S28969.
DR PDB; INBA; 22-JUN-94.
KW HYDROLASE; 3D-STRUCTURE.
FT ACT_SITE 177 177 INVOLVED IN HYDROLYSIS OF THE SUBSTRATE.
SQ SEQUENCE 264 AA; 29057 MW; 81A56865 CRC32;

Query Match 40.4%; Score 57; DB 2; Length 264;
Best Local Similarity 40.0%; Pred. No. 4.57e-01;
Matches 6; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Db 171 gataagcvrhtveda 185
QY 6 GTKSKCVQKV 20
I:::|||||:::

RESULT 7
ID SP70_DICDI STANDARD; PRT; 537 AA.
AC P15269; P08126;
DT 01-AUG-1988 (REL. 08, CREATED)
DT 01-APR-1990 (REL. 14, LAST SEQUENCE UPDATE)
DT 01-FEB-1994 (REL. 28, LAST ANNOTATION UPDATE)
DE SPORE COAT PROTEIN SP70 PRECURSOR (BEEJIN PROTEIN).
GN COTB.
OS DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).
OC EUKARYOTA; PROTOZOA; SARCOMASTIGOPHORA; SARCODINA; RHIZOPODA;
OC EUMYCETOZOA; DICTYOSTELIA.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 90097939.
RA FOSNAUGH K.L., LOOMIS W.F.;
RL MOL. CELL. BIOL. 9:5215-5218(1989).
RN [2]
RP PRELIMINARY SEQUENCE OF 72-170 FROM N.A.

```

```

RX MEDLINE; 87057653.
RA GOMER R.H., DATTA S., FIRTEL R.A.;
RL J. CELL BIOL. 103:1999-2015(1986).
DR EMBL; M26238; G167889; -.
DR PIR; B33485; B33485.
DR PIR; B25439; B25439.
DR DICTYDB; DD03009; COTB.
KW GLYCOPROTEIN; PHOSPHORYLATION; REPEAT; SPORULATION; SIGNAL.
FT SIGNAL 1 20
FT CHAIN 21 537 SPORE COAT PROTEIN SP70.
FT DOMAIN 182 250 SER/THR-RICH.
FT DOMAIN 190 248 5.5 X 11 AA TANDEM REPEATS.
FT REPEAT 190 200 1.
FT REPEAT 191 211 2.
FT REPEAT 212 222 3.
FT REPEAT 223 233 4.
FT REPEAT 234 244 5.
FT REPEAT 245 248 6 (INCOMPLETE).
FT REPEAT 256 263 PRESPORE MOTIF.
FT REPEAT 284 291 PRESPORE MOTIF.
FT REPEAT 364 371 PRESPORE MOTIF.
FT CARBOHYD 97 97 POTENTIAL.
SQ SEQUENCE 537 AA; 56650 MW; 5D59CBAC CRC32;

Query Match 39.7%; Score 56; DB 9; Length 537;
Best Local Similarity 54.5%; Pred. No. 7.54e-01;
Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Db 291 kngecirckve 301
QY 8 KSKKCVQKV 18
I:::|||||:::

RESULT 8
ID GLB1_MAIZE STANDARD; PRT; 573 AA.
AC P15590;
DT 01-APR-1990 (REL. 14, CREATED)
DT 01-AUG-1990 (REL. 15, LAST SEQUENCE UPDATE)
DT 01-OCT-1994 (REL. 30, LAST ANNOTATION UPDATE)
DE GLOBULIN-1 S ALLELE PRECURSOR (GLB1-S) (/S-LIKE).
GN GLB1.
OS ZEA MAYS (MAIZE).
OC EUKARYOTA; PLANTA; EMBRYOPHYTA; ANGIOSPERMAE; MONOCOTYLEDONEAE;
OC CYPERALES; GRAMINEAE.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. INBRED LINE VA26;
RA BELANGER F.C., KRIZ A.L.;
RL PLANT PHYSIOL. 91:636-643(1989).
RN [2]
RP SEQUENCE OF 87-100.
RX MEDLINE; 89374022.
RA KRIZ A.L.;
RL BIOCHEM. GENET. 27:239-251(1989).
CC -1- SIMILARITY: TO OTHER 7S SEED STORAGE PROTEINS (PHASEOLIN, VICILIN,
CC CONVICILIN, CONGLICININ, ETC.).
CC -1- POLYMORPHISM: THE THREE MOST COMMONLY OCCURRING GLB1 ALLELES HAVE
CC THE DESIGNATION L, I, AND S FOR LARGE, INTERMEDIATE, AND SMALL
CC PROTEINS, RESPECTIVELY.
CC -1- PTM: THREE PROTEIN-PROCESSING STEPS OCCUR IN THE FORMATION OF THE
CC MATURE PROTEIN FROM THE PRIMARY TRANSLATION PRODUCT.
DR EMBL; M24845; G168481; -.
DR HSSP; P02853; 1CAU.
DR MAIZEDB; 30181; -.
KW SEED STORAGE PROTEIN; SIGNAL. OR 21 (POTENTIAL).
FT SIGNAL 1 18
FT PROPEP 19 86
FT CHAIN 87 573 GLOBULIN-1 S.
FT CARBOHYD 349 349 POTENTIAL.
SQ SEQUENCE 573 AA; 65029 MW; 7E755E20 CRC32;

Query Match 39.7%; Score 56; DB 4; Length 573;
Best Local Similarity 58.3%; Pred. No. 7.54e-01;

```

Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Db 32 hghksgvrr 43
| | | | | | | | | |
QY 4 HOGTKSKCVRQ 15

RESULT 9
ID RPOB.PSEPU STANDARD; PRT; 1357 AA.
AC P19175;
DT 01-NOV-1990 (REL. 16, CREATED)
DT 01-MAR-1992 (REL. 21, LAST SEQUENCE UPDATE)
DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
DE DNA-DIRECTED RNA POLYMERASE BETA CHAIN (EC 2.7.7.6) (TRANSCRIPTASE
DE BETA CHAIN) (RNA POLYMERASE BETA SUBUNIT).
GN RPOB.
OS PSEUDOMONAS PUTIDA.
OC PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; AEROBIC RODS AND COCCI;
OC PSEUDOMONADACEAE.
RN [1]
RN SEQUENCE FROM N.A.
RA BORODIN A.M., DANILKOVICH A.V., ALLIKMETTS R.L., ROSTAPSHOV V.M.,
RA CHERNOV I.P., AZHYKINA T.L., MONASTYRSKAYA S., SVERDLOV D.;
RL DOKL. BIOCHEM. 302:1261-1265(1988).
RN [2]
RN SEQUENCE OF 1036-1357 FROM N.A.
RX MEDLINE; 89117617.
RA BORODIN A.M., DANILKOVICH A.V., CHERNOV I.P., AZHYKINA T.L.,
RA ROSTAPSHOV V.M., MONASTYRSKAYA G.S.;
RL BIOORG. KHIM. 14:1179-1182(1988).
CC -!- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION
CC OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
CC SUBSTRATES.
CC -!- CATALYTIC ACTIVITY: N NUCLEOSIDE TRIPHOSPHATE - N PYROPHOSPHATE +
CC RNA(N).
CC -!- SUBUNIT: THE ENZYME CONSISTS OF THE SIGMA CHAIN AND THE CORE
CC ENZYME WHICH IS COMPOSED OF 2 ALPHA CHAINS, 1 BETA CHAIN, AND 1
CC BETA' CHAIN.
CC -!- SIMILARITY: BELONGS TO THE RNA POLYMERASE BETA CHAIN FAMILY.
DR EMBL; X15849; G45729; -.
DR EMBL; M38319; G151547; -.
KW TRANSCRIPTION; DNA-DIRECTED RNA POLYMERASE.
FT CONFLICT 1180 1180 T -> N (IN REF. 2).
FT CONFLICT 1184 1184 I -> V (IN REF. 2).
FT CONFLICT 1236 1236 F -> S (IN REF. 2).
SQ SEQUENCE 1357 AA; 151305 MW; BBF88A37 CRC32;

Query Match 39.7%; Score 56; DB 8; Length 1357;
Best Local Similarity 41.2%; Pred. No. 7.54e-01;
Matches 7; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

Db 450 idhlgncrvvcmgmae 466
| | | | | | | | | |
QY 2 IDHGTSSKCVRKVE 18

RESULT 10
ID YTX1.XENLA STANDARD; PRT; 775 AA.
AC P14380;
DT 01-JAN-1990 (REL. 13, CREATED)
DT 01-JAN-1990 (REL. 13, LAST SEQUENCE UPDATE)
DT 01-APR-1990 (REL. 14, LAST ANNOTATION UPDATE)
DE TRANSPOSON TX1 HYPOTHETICAL 82 KD PROTEIN (ORF 1).
OS XENOPUS LAEVIS (AFRICAN CLAWED FROG).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; AMPHIBIA; ANURA.
RN [1]
RN SEQUENCE FROM N.A.
RX MEDLINE; 89384562.
RA GARRETT J.E., KNUSTZON D.S., CARROLL D.;
RL MOL. CELL. BIOL. 9:3018-3027(1989).
DR EMBL; M26915; G214845; -.
DR PIR; A32494; A32494.
KW HYPOTHETICAL PROTEIN; TRANSPOSABLE ELEMENT.

SQ SEQUENCE 775 AA; 82355 MW; 9738B05A CRC32;

Query Match 39.0%; Score 55; DB 11; Length 775;
Best Local Similarity 46.7%; Pred. No. 1.24e+00;
Matches 7; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Db 617 sntskcvssvegtpt 631
| | | | | | | | | |
QY 7 TKSSKCVRKVEGSS 21

RESULT 11
ID COTZ.BACSU STANDARD; PRT; 148 AA.
AC Q08312;
DT 01-OCT-1994 (REL. 30, CREATED)
DT 01-OCT-1994 (REL. 30, LAST SEQUENCE UPDATE)
DT 01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)
DE SPORE COAT PROTEIN 2.
GN COTZ.
OS BACILLUS SUBTILIS.
OC PROKARYOTA; FIRMICUTES; ENDOSPORE-FORMING RODS AND COCCI; BACILLACEAE.
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN-168 / JH642;
RX MEDLINE; 93285989.
RA ZHANG J., FITZ-JAMES P.C., ARONSON A.I.;
RL J. BACTERIOL. 175:3757-3766(1993).
CC -!- SUBCELLULAR LOCATION: SPORE OUTER COAT.
CC -!- SUBUNIT: DISULFIDE CROSS-LINKED EITHER TO ITSELF OR TO COTY.
CC -!- SIMILARITY: TO COTY.
DR EMBL; L10116; G304149; -.
DR PIR; E47119; E47119.
DR SUBTILIST; BG10500; COTZ.
KW SPORULATION.
SQ SEQUENCE 148 AA; 16534 MW; B5442F5E CRC32;

Query Match 38.3%; Score 54; DB 2; Length 148;
Best Local Similarity 63.6%; Pred. No. 2.01e+00;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Db 4 ktsscvreave 14
| | | | | | | | | |
QY 8 KSSKCVRKVE 18

RESULT 12
ID DAP2.YEAST STANDARD; PRT; 818 AA.
AC P18962;
DT 01-NOV-1990 (REL. 16, CREATED)
DT 01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
DT 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
DE DIPEPTIDYL AMINOPEPTIDASE B (EC 3.4.14.-) (DPAP B) (YSCV).
GN DAP2 OR YHR028C.
OS SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
OC EUKARYOTA; FUNGI; ASCOMICOTINA; HEMIASCOMYCETES.
RN [1]
RN SEQUENCE FROM N.A.
RX MEDLINE; 89174971.
RA ROBERTS C.J., POHLIG G., ROTHMAN J.H., STEVENS T.H.;
RL J. CELL BIOL. 108:1363-1373(1989).
RN [2]
RN SEQUENCE FROM N.A.
RC STRAIN-S288C / AB972;
RX MEDLINE; 94378003.
RA JOHNSTON M., ANDREWS S., BRINKMAN R., COOPER J., DING H., DOVER J.,
RA DU Z., FAVELLO A., FULTON L., GATTUNG S., GEISEL C., KIRSTEN J.,
RA KUCABA T., HILLIER L., JIER M., JOHNSTON L., LANGSTON Y.,
RA LATREILLE P., LOUIS E.J., MACRI C., MARIS E., MENEZES S., MOUSER L.,
RA NHAN M., RIFKIN L., RILES L., ST PETER H., TREVASKIS E., VAUGHAN K.,
RA VIGNATI D., WILCOX L., WOHLDMAN P., WATERSTON R., WILSON R.,
RA VAUDIN M.;
RL SCIENCE 265:2077-2082(1994).

CC -!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. LYSOSOME-LIKE

CC VACUOLES.
 CC -!- SIMILARITY: TO DPAP A.
 CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S9B; ALSO KNOWN AS THE
 CC PROLYL OLIGOPEPTIDASE FAMILY.
 DR EMBL; X15484; G3660; -.
 DR EMBL; U10399; G500698; -.
 DR PIR; A30107; A30107.
 DR PIR; S46780; S46780.
 DR LISTA; SC00265; DAP2.
 DR SGD; L0000483; DAP2.
 DR PROSITE; PS00708; PRO_ENDOPEP_SER.
 DR HYDROLASE; DIPEPTIDASE; SERINE PROTEASE; TRANSMEMBRANE; GLYCOPROTEIN;
 KW SIGNAL-ANCHOR.
 FT DOMAIN 1 29
 FT TRANSMEM 30 45
 FT DOMAIN 46 818
 FT ACT_SITE 679 756
 FT ACT_SITE 756 789
 FT ACT_SITE 789 789
 FT CARBOHYD 63 63
 FT CARBOHYD 79 79
 FT CARBOHYD 110 110
 FT CARBOHYD 139 139
 FT CARBOHYD 372 372
 FT CARBOHYD 392 392
 FT CARBOHYD 421 421
 FT CARBOHYD 738 738
 FT CONFLICT 83 83
 FT CONFLICT 125 125
 FT CONFLICT 182 188
 FT CONFLICT 200 200
 FT CONFLICT 366 375
 FT CONFLICT 808 818
 FT SEQUENCE 818 AA; 93404 MW; 8D658EBB CRC32;
 Query Match 38.3%; Score 54; DB 3; Length 818;
 Best Local Similarity 33.3%; Pred. No. 2.01e+00;
 Matches 7; Conservative 7; Mismatches 7; Indels 0; Gaps 0;
 Db 511 lvdhfrkaekcdkgnvlgks 531
 QY 1 VIDHQGTSSKCKVRQKVEGS 21
 RESULT 13
 ID YR7L_CAEEL STANDARD; PRT; 1039 AA.
 AC Q09564;
 DT 01-NOV-1995 (REL. 32, CREATED)
 DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
 DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
 DE HYPOTHETICAL 118.2 KD PROTEIN F43C1.1 IN CHROMOSOME III.
 GN F43C1.1.
 OS CAENORHABDITIS ELEGANS.
 OC EUKARYOTA; METAZOA; ACOLLOMATES; NEMATODA; SECERNENTEIA; RHABDITIDA.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RA JASSAL B.;
 RP SUBMITTED (DEC-1994) TO EMBL/GENBANK/DBJ DATA BANKS.
 CC -!- SIMILARITY: THE REPEATED LEUCINE-RICH (LRR) SEGMENT IS FOUND IN
 CC -!- MANY PROTEINS. NUMBER IN THIS PROTEIN: 3.
 CC -!- SIMILARITY: CONTAINS A PP2C-LIKE DOMAIN.
 DR EMBL; Z46937; G603526; -.
 DR WORMPEP; F43C1.1; CE01582.
 KW HYPOTHETICAL PROTEIN; LEUCINE-REPEAT; REPEAT.
 FT DOMAIN 216 284
 FT REPEAT 216 238
 FT REPEAT 239 261
 FT REPEAT 262 284
 FT DOMAIN 669 903
 FT SEQUENCE 1039 AA; 118182 MW; 877F95CB CRC32;

Query Match 38.3%; Score 54; DB 11; Length 1039;
 Best Local Similarity 38.1%; Pred. No. 2.01e+00;
 Matches 8; Conservative 5; Mismatches 7; Indels 1; Gaps 1;
 Db 677 vsgsrgrmkknkcirvrvent 697
 QY 1 VIDHQGTSSKCKVRQ-KVEGS 20
 RESULT 14
 ID E411_ADE05 STANDARD; PRT; 116 AA.
 AC P04489;
 DT 13-AUG-1987 (REL. 05, CREATED)
 DT 13-AUG-1987 (REL. 05, LAST SEQUENCE UPDATE)
 DT 01-WAR-1992 (REL. 21, LAST ANNOTATION UPDATE)
 DE PROBABLE EARLY E4 11 KD PROTEIN.
 OS HUMAN ADENOVIRUS TYPE 5.
 OC VIRIDAE; DS-DNA NONENVELOPED VIRUSES; ADENOVIRIDAE; MASTADENOVIRUSES.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 83164198.
 RA SARNOW P.; HEARING P.; ANDERSON C.W.; REICH N.; LEVINE A.J.;
 RL J. MOL. BIOL. 162:565-583(1982).
 RN [2]
 RP COMPLETE GENOME.
 RX MEDLINE; 92087470.
 RA CHROBOCZEK J.; BIEBER F.; JACROT B.;
 RL VIROLOGY 186:280-285(1992).
 DR EMBL; M73260; -; NOT_ANNOTATED_CDS.
 DR EMBL; X02998; G58502; -.
 DR PIR; B03807; Q4ADE5.
 KW EARLY PROTEIN
 SQ SEQUENCE 116 AA; 13298 MW; 66EA9B5C CRC32;
 Query Match 37.6%; Score 53; DB 3; Length 116;
 Best Local Similarity 60.0%; Pred. No. 3.25e+00;
 Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 Db 3 rclrlkvega 12
 QY 11 KCVQRKVEGS 20
 RESULT 15
 ID E411_ADE02 STANDARD; PRT; 116 AA.
 AC P03241;
 DT 21-JUL-1986 (REL. 01, CREATED)
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
 DT 01-APR-1990 (REL. 14, LAST ANNOTATION UPDATE)
 DE PROBABLE EARLY E4 11 KD PROTEIN.
 OS HUMAN ADENOVIRUS TYPE 2.
 OC VIRIDAE; DS-DNA NONENVELOPED VIRUSES; ADENOVIRIDAE; MASTADENOVIRUSES.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 82059444.
 RA HERISSE J.; RIGOLET M.; DUPONT DE DINECHIN S.; GALIBERT F.;
 RL NUCLEIC ACIDS RES. 9:4023-4042(1981).
 DR EMBL; J01917; G209839; -.
 DR PIR; A03807; Q4ADE2.
 KW EARLY PROTEIN
 SQ SEQUENCE 116 AA; 13255 MW; 950D6981 CRC32;
 Query Match 37.6%; Score 53; DB 3; Length 116;
 Best Local Similarity 60.0%; Pred. No. 3.25e+00;
 Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 Db 3 rclrlkvega 12
 QY 11 KCVQRKVEGS 20
 RESULT 16
 ID GRN_MOUSE STANDARD; PRT; 589 AA.

P28798;
 01-DEC-1992 (REL. 24, CREATED)
 01-OCT-1994 (REL. 30, LAST SEQUENCE UPDATE)
 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
 GRANULINS PRECURSOR (ACROGRANIN).
 GRN.
 OS MUS MUSCULUS (MOUSE).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; RODENTIA.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 93245991.
 RA BABA T., NEMOTO H., WATANABE K., ARAI Y., GERTON G.L.;
 RL FEBS LETT. 322:89-94(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE-KIDNEY;
 RX MEDLINE; 92317004.
 RA FLOWMAN G.D., GREEN I.M., NEUBAUER M.G., BUCKLEY S., MCDONALD V.L.,
 RA TODARO G.I., SHOYAB M.;
 RL J. BIOL. CHEM. 267:13073-13078(1992).
 RN [3]
 RP FUNCTION: GRANULINS HAVE POSSIBLE CYTOKINE-LIKE ACTIVITY. THEY MAY
 CC PLAY A ROLE IN INFLAMMATION, WOUND REPAIR, AND TISSUE REMODELING.
 CC -1- PPM: GRANULINS ARE DISULFIDE BRIDGED.
 CC -1- TISSUE SPECIFICITY: UBIQUITOUS.
 DR EMBL; D16195; G286068; -;
 DR EMBL; M85736; G191767; -;
 DR EMBL; X62321; G50852; -;
 DR EMBL; S59740; -; NOT_ANNOTATED_CDS.
 DR PROSITE; PS00799; GRANULINS.
 KW CYTOKINE; REPEAT; GLYCOPROTEIN; SIGNAL.
 FT SIGNAL 1 17
 FT CHAIN 18 589
 FT PEPTIDE 758 7113
 FT PEPTIDE 7122 7178
 FT PEPTIDE 205 260
 FT PEPTIDE 280 334
 FT PEPTIDE 362 7414
 FT PEPTIDE 440 7493
 FT PEPTIDE 7517 7568
 FT CARBOHYD 38 38
 FT CARBOHYD 263 263
 FT CARBOHYD 373 373
 FT CARBOHYD 526 526
 FT CONFLICT 350 350
 SQ SEQUENCE 589 AA; 63458 MW; 96FD3D02 CRC32;
 Query Match 37.6%; Score 53; DB 4; Length 589;
 Best Local Similarity 35.7%; Pred. No. 3.25e+00;
 Matches 5; Conservative 7; Mismatches 2; Indels 0; Gaps 0;
 Db 560 hcsargtkclrkki 573
 QY 4 HQGKSSKCYRQKV 17
 RESULT 17
 ID GALC_HUMAN STANDARD; PRT; 669 AA.
 AC P54803;
 DT 01-OCT-1996 (REL. 34, CREATED)
 DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
 DE GALACTOCEREBROSIDASE PRECURSOR (EC 3.2.1.46) (GALCERASE)
 DE (GALACTOSYLCEAMIDASE) (GALACTOSYLCEAMIDE BETA-GALACTOSIDASE)
 DE (GALACTOCEREBROSIDE BETA-GALACTOSIDASE).
 GN GALC.
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; PRIMATES.
 RN [1]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RC TISSUE-PLACENTA, AND SKIN FIBROBLAST;
 RX MEDLINE; 94128088.

RA SAKAI N., INUI K., FUJII N., FUKUSHIMA H., NISHIMOTO J.,
 RA YANAGIHARA I., ISEGAWA Y., IWAMATSU A., OKADA S.;
 RL BIOCHEM. BIOPHYS. RES. COMMUN. 198:485-491(1994).
 RN [2]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 27-59 AND 436-454.
 RC TISSUE-BRAIN, AND TESTIS;
 RX MEDLINE; 94108435.
 RA CHEN Y.Q., RAFI M.A., DE GALA G., WENGER D.A.;
 RL HUM. MOL. GENET. 2:1841-1845(1993).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 95324938.
 RA LUZI P., RAFI M.A., WENGER D.A.;
 RL GENOMICS 26:407-409(1995).
 RN [4]
 RP SEQUENCE OF 27-45; 436-454, AND CHARACTERIZATION.
 RC TISSUE-URINE;
 RX MEDLINE; 94002192.
 RA CHEN Y.Q., WENGER D.A.;
 RL BIOCHIM. BIOPHYS. ACTA 1170:53-61(1993).
 RN [5]
 RP VARIANTS GLD ALA-302 AND GLY-550.
 RA TATSUMI N., INUI K., SAKAI N., FUKUSHIMA H., NISHIMOTO J.,
 RA YANAGIHARA I., NISHIGAKI T., TSURAMOTO H., FU L., TANIKE M.,
 RA OKADA S.;
 RL HUM. MOL. GENET. 45:1865-1868(1995).
 CC -1- FUNCTION: HYDROLYSES THE GALACTOSE ESTER BONDS OF
 CC GALACTOSYLCEAMIDE, GALACTOSYLSPHINGOSINE, LACTOSYLCEAMIDE, AND
 CC MONOGALACTOSYDIGLYCERIDE. ENZYME WITH VERY LOW ACTIVITY
 CC RESPONSIBLE FOR THE LYSOSOMAL CATABOLISM OF GALACTOSYLCEAMIDE, A
 CC MAJOR LIPID IN MYELIN, KIDNEY AND EPITHELIAL CELLS OF SMALL
 CC INTESTINE AND COLON. HAS AN OPTIMAL PH BETWEEN 4.0 AND 4.4.
 CC ACTIVITY IS LOST WHEN HEATED AT 52 DEGREES CELSIUS FOR FIVE
 CC MINUTES.
 CC -1- CATALYTIC ACTIVITY: D-GALACTOSYL-N-ACYLSPHINGOSINE + H(2)O - D-
 CC GALACTOSE + N-ACYLSPHINGOSINE.
 CC -1- SUBCELLULAR LOCATION: LYSOSOMAL.
 CC -1- TISSUE SPECIFICITY: HIGHEST LEVEL OF ACTIVITY IN TESTES COMPARED
 CC TO BRAIN, KIDNEY, PLACENTA AND LIVER. CAN ALSO BE FOUND IN URINE.
 CC -1- ALTERNATIVE PRODUCTS: TWO FORMS ARE PRODUCED BY ALTERNATIVE
 CC SPLICING. THE SEQUENCE SHOWN HERE IS THAT OF THE LONG FORM.
 CC -1- DISEASE: DEFECTS IN GALC ARE THE CAUSE OF GLOBOID CELL
 CC LEUKODISTROPHY (GLD) (OR KRABBE DISEASE), AN AUTOSOMAL RECESSIVE
 CC DISORDER CHARACTERIZED BY HYPERTONICITY, IRRITABILITY,
 CC INTELLECTUAL DELAY AND REGRESSION WITHIN THE FIRST SIX MONTHS OF
 CC LIFE. THE AVERAGE AGE AT DEATH IS THIRTEEN MONTHS, ALTHOUGH LATER
 CC ONSET FORMS HAVE BEEN IDENTIFIED. BIOCHEMICALLY GALC DEFICIENCY
 CC RESULTS IN AN ABNORMAL AND/OR INSUFFICIENT PRODUCTION OF MYELIN.
 CC -1- SIMILARITY: BELONGS TO FAMILY 59 OF GLYCOSYL HYDROLASES.
 DR EMBL; D25283; G457444; -;
 DR EMBL; D25284; G457446; -;
 DR EMBL; L23116; G431310; -;
 DR EMBL; L38559; G710535; -;
 DR EMBL; L38544; G710535; JOINED.
 DR EMBL; L38545; G710535; JOINED.
 DR EMBL; L38546; G710535; JOINED.
 DR EMBL; L38547; G710535; JOINED.
 DR EMBL; L38548; G710535; JOINED.
 DR EMBL; L38549; G710535; JOINED.
 DR EMBL; L38550; G710535; JOINED.
 DR EMBL; L38551; G710535; JOINED.
 DR EMBL; L38552; G710535; JOINED.
 DR EMBL; L38553; G710535; JOINED.
 DR EMBL; L38554; G710535; JOINED.
 DR EMBL; L38555; G710535; JOINED.
 DR EMBL; L38556; G710535; JOINED.
 DR EMBL; L38557; G710535; JOINED.
 DR EMBL; L38558; G710535; JOINED.
 DR MIN; 245200; -;
 KW HYDROLASE; GLYCOSIDASE; GLYCOPROTEIN; SIGNAL; ALTERNATIVE SPLICING;
 KW DISEASE MUTATION.
 FT SIGNAL 1 26
 FT CHAIN 27 669
 FT CARBOHYD 127 127
 FT GALACTOCEREBROSIDASE.
 FT POTENTIAL.

FT CARBOHYD 363 363 POTENTIAL.
 FT CARBOHYD 387 387 POTENTIAL.
 FT CARBOHYD 540 540 POTENTIAL.
 FT CARBOHYD 543 543 POTENTIAL.
 FT CARBOHYD 586 586 POTENTIAL.
 FT VARSPLIC 372 392 SHKSKCIRPPLPYNVSQQ ->
 MISSING (IN SHORT FORM).
 FT VARSPLIC 393 669 VNFCCCWINSLLYWRNKI (IN SHORT FORM).
 FT VARIANT 302 302 P -> A (IN GLD).
 FT VARIANT 550 550 V -> G (IN GLD).
 FT CONFLICT 546 546 I -> T (IN REF. 3).
 SQ SEQUENCE 669 AA; 75147 MW; 9EF9402F CRC32;

Query Match 37.6%; Score 53; DB 4; Length 669;
 Best Local Similarity 42.9%; Pred. No. 3.25e+00;
 Matches 6; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Db 367 iletshkhskcrlr 380
 : : : : :
 QY 1 VIDHQGTSSKRCVR 14

RESULT 18
 ID PGDS_HUMAN STANDARD; PRT; 1089 AA.
 AC P16234;
 DT 01-APR-1990 (REL. 14, CREATED)
 DT 01-APR-1990 (REL. 14, LAST SEQUENCE UPDATE)
 DT 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
 DE ALPHA PLATELET-DERIVED GROWTH FACTOR RECEPTOR PRECURSOR
 DE (EC 2.7.1.112).
 GN PDGFRA.
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; PRIMATES.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 89130149.
 RA MATSUI T., HEIDARAN M., MIKI T., POPESCU N., LA ROCHELLE W.,
 RA KRAUS M., PIERCE J., ARONSON S.;
 RL SCIENCE 243:800-804 (1989).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 89296915.
 RA CLAESON-WELSH L., ERIKSSON A., WESTERMARK B., HELDIN C.H.;
 RL PROC. NATL. ACAD. SCI. U.S.A. 86:4917-4921 (1989).
 CC -!- FUNCTION: THIS RECEPTOR BINDS PLATELET-DERIVED GROWTH FACTOR AND
 HAS A TYROSINE-PROTEIN KINASE ACTIVITY. THIS RECEPTOR CAN BIND
 EITHER PDGF-A OR PDGF-B.
 CC -!- SUBUNIT: DIMER OF EITHER ALPHA-ALPHA, BETA-BETA OR ALPHA-BETA
 SUBUNITS.
 CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -!- SIMILARITY: BELONGS TO THE CSF-1/PDGF RECEPTOR FAMILY OF TYROSINE-
 PROTEIN KINASES.
 CC -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. THE
 EXTRACELLULAR DOMAIN CONTAINS FIVE IG-FOLD DOMAINS.
 DR EMBL; M21574; G189734; -.
 DR EMBL; M22734; G189726; -.
 DR PIR; A40162; PFHUGA.
 DR MIN; 173490; -.
 DR PROSITE; PS00107; PROTEIN KINASE ATP.
 DR PROSITE; PS00109; PROTEIN KINASE TYR.
 DR PROSITE; PS00240; RECEPTOR_TYR_KIN_III.
 DR PROSITE; PS00011; PROTEIN_KINASE_DOM.
 KW TYROSINE-PROTEIN KINASE; RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN;
 KW TRANSFERASE; PHOSPHORYLATION; ATP-BINDING; IMMUNOGLOBULIN FOLD;
 KW SIGNAL.
 FT SIGNAL 1 23 ALPHA PLATELET-DERIVED GROWTH FACTOR
 FT CHAIN 24 1089 RECEPTOR.
 FT DOMAIN 24 524 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 525 549 POTENTIAL.
 FT DOMAIN 550 1089 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 593 954 PROTEIN KINASE.

FT DOMAIN 1041 1087 SER-RICH.
 FT NP_BIND 599 607 ATP (BY SIMILARITY).
 FT BINDING 627 627 ATP (BY SIMILARITY).
 FT ACT_SITE 818 818 BY SIMILARITY.
 FT MOD_RES 849 849 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
 FT CARBOHYD 42 42 POTENTIAL.
 FT CARBOHYD 76 76 POTENTIAL.
 FT CARBOHYD 103 103 POTENTIAL.
 FT CARBOHYD 179 179 POTENTIAL.
 FT CARBOHYD 353 353 POTENTIAL.
 FT CARBOHYD 359 359 POTENTIAL.
 FT CARBOHYD 458 458 POTENTIAL.
 FT CARBOHYD 468 468 POTENTIAL.
 SQ SEQUENCE 1089 AA; 122669 MW; 43E6902A CRC32;

Query Match 37.6%; Score 53; DB 7; Length 1089;
 Best Local Similarity 38.1%; Pred. No. 3.25e+00;
 Matches 8; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

Db 421 vddhghstggqvtvrcatgtp 441
 : : : : :
 QY 1 VIDHQGTSSKRCVRQVEGSS 21

RESULT 19
 ID ESG2_TRYBB STANDARD; PRT; 329 AA.
 AC P04478;
 DT 13-AUG-1987 (REL. 05, CREATED)
 DT 13-AUG-1987 (REL. 05, LAST SEQUENCE UPDATE)
 DT 01-MAY-1992 (REL. 22, LAST ANNOTATION UPDATE)
 DE VSG EXPRESSION SITE-ASSOCIATED PROTEIN 221A PRECURSOR (ESAG PROTEIN).
 OS TRYPAOSOMA BRUCEI BRUCEI.
 OC EUKARYOTA; PROTOZOA; SARCOMASTIGOPHORA; NASTIGOPHORA; KINETOPLASTIDA;
 OC TRYPAOSOMATIDAE.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 85254917.
 RA CULLY D.F., IP H.S., CROSS G.A.M.;
 RL CELL 42:173-182 (1985).
 CC -!- FUNCTION: NOT KNOWN BUT MAY BE RELATED TO ACTIVATION OF THE
 VARIANT SURFACE GLYCOPROTEIN GENES.
 DR EMBL; M11452; G162073; -.
 DR PIR; A03395; VNUT21.
 KW SIGNAL 1 23 VSG EXPRESSION SITE-ASSOCIATED PROTEIN
 FT CHAIN 24 329 221A.
 FT CARBOHYD 73 73 POTENTIAL.
 FT CARBOHYD 294 294 POTENTIAL.
 FT CARBOHYD 308 308 POTENTIAL.
 SQ SEQUENCE 329 AA; 36603 MW; 6B9966CE CRC32;

Query Match 36.9%; Score 52; DB 3; Length 329;
 Best Local Similarity 70.0%; Pred. No. 5.22e+00;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Db 176 akcysqskveg 185
 : : : : :
 QY 10 SKCVRQKVEG 19

RESULT 20
 ID OCD_AGR75 STANDARD; PRT; 354 AA.
 AC P09773;
 DT 01-MAR-1989 (REL. 10, CREATED)
 DT 01-MAR-1989 (REL. 10, LAST SEQUENCE UPDATE)
 DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
 DE ORNITHINE CYCLODEAMINASE (EC 4.3.1.12) (OCD).
 GN OCD.
 OS AGROBACTERIUM TUMEFACIENS.
 OG PLASMID TIC58.
 OC PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; AEROBIC RODS AND COCCI;
 OC RHIZOBIACEAE.

```

RN SEQUENCE FROM N.A.
RP MEDLINE; 88185308.
RA SANS N., SCHINDLER U., SCHROEDER J.;
RL EUR. J. BIOCHEM. 173:123-130(1988).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE; 94321320.
RA ZANKER H., LURZ G., LANGRIDGE U., LANGRIDGE P., KREUSCH D.,
RJ SCHROEDER J.;
RL J. BACTERIOL. 176:4511-4517(1994).
CC -1- CATALYTIC ACTIVITY: L-ORNITHINE = L-PROLINE + NH(3).
CC -1- PATHWAY: LAST STEP IN THE TI-PLASMIID-CODED PATHWAY FROM NOPALINE
CC TO PROLINE.
CC -1- ENZYME REGULATION: ACTIVITY IS SUBJECT TO SUBSTRATE INHIBITION, IS
CC STIMULATED BY NAD(+). (PRESUMABLY ACTING AS A CATALYTIC COFACTOR)
CC AND IS REGULATED BY L-ARGININE.
CC -1- SIMILARITY: REGIONS OF SIMILARITY WITH E.COLI AND P.AERUGINOSA
CC CARBAMOYLTRANSFERASES.
DR EMBL; X07435; G39108; -.
DR EMBL; Z30316; G496538; -.
DR PIR; S00402; PLASMIID.
KW LASE; NAD; PLASMIID.
FT DOMAIN 172 207
FT REGION OF SUBSTRATE-BINDING SITE
FT (POTENTIAL).
SQ SEQUENCE 354 AA; 36984 MW; 6F310E2E CRC32;

Query Match 36.9%; Score 52; DB 7; Length 354;
Best Local Similarity 63.6%; Pred. No. 5.22e+00;
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Db 312 ryvdrvegs 322
: ||: |||||
Qy 11 KCVRQKVEGS 21

RESULT 21
ID P2X5_RAT STANDARD; PRT; 455 AA.
AC P51578;
DT 01-OCT-1996 (REL. 34, CREATED)
DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE P2X PURINOCEPTOR 5 (ATP RECEPTOR) (P2X5) (PURINERGIC RECEPTOR).
GN P2X5.
OS RATTUS NORVEGICUS (RAT).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-COEELIAC GANGLION;
RX MEDLINE; 96256686.
RA COLLO G., KAWASHIMA E., PICH E., NEIDHART S., NORTH R.A.,
RA SURPRENANT A., BUELL G.N.;
RL J. NEUROSCI. 16:2495-2507(1996).
CC -1- FUNCTION: RECEPTOR FOR ATP THAT ACTS AS A LIGAND GATED ION
CC CHANNEL.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- SUBUNIT: HOMO- OR HETEROPOLYMERS (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE P2X RECEPTOR FAMILY.
DR EMBL; X92069; E205287; -.
KW IONIC CHANNEL; TRANSMEMBRANE; ION TRANSPORT; RECEPTOR; GLYCOPROTEIN.
FT DOMAIN 1 30 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 31 51 1 (POTENTIAL).
FT DOMAIN 52 341 EXTRACELLULAR, CYSTEINE-RICH (POTENTIAL).
FT TRANSMEM 342 362 2 (POTENTIAL).
FT DOMAIN 363 455 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 77 77 POTENTIAL.
FT CARBOHYD 157 157 POTENTIAL.
FT CARBOHYD 202 202 POTENTIAL.
SQ SEQUENCE 455 AA; 51479 MW; 7EDE74C3 CRC32;

Query Match 36.9%; Score 52; DB 7; Length 455;
Best Local Similarity 35.7%; Pred. No. 5.22e+00;

```

```

Matches 5; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

Db 141 vvaghglktgrclr 154
: :| |::| |
Qy 1 VIDHOGTRSSKRCVR 14

RESULT 22
ID YIF2_YEAST STANDARD; PRT; 121 AA.
AC P40525;
DT 01-FEB-1995 (REL. 31, CREATED)
DT 01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE PROBABLE 60S RIBOSOMAL PROTEIN YIL052C.
GN YIL052C.
OS SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
OC EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOCYCETES.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-S288C / AB972;
RA BARRELL B.G., BADCOCK K., BANKIER A.T., BOWMAN S., BROWN D.,
RA CHURCHER C.M., CONNOR R., COPSEY T., DEAR S., DEVLIN K., FRASER A.,
RA GENTLES S., HAMLYN N., HORSNELL T.S., HUNT S., JAGELS K., JONES M.,
RA LOUIS E., LYE G., MOULE S., MOULE T., ODELL C., PEARSON D.,
RA RAJANDREAM M.A., RILES L., ROWLEY N., SKELTON J., SMITH V.,
RA WALSH S.V., WHITEHEAD S.;
RL SUBMITTED (DEC-1994) TO EMBL/GENBANK/DDBJ DATA BANKS.
CC -1- SIMILARITY: BELONGS TO THE L34E FAMILY OF RIBOSOMAL PROTEINS.
DR EMBL; Z38060; G557816; -.
DR EMBL; Z47047; G763294; -.
DR PIR; S48427; S48427.
DR PROSITE; PS01145; RIBOSOMAL_L34E_1.
DR PROSITE; PS01146; RIBOSOMAL_L34E_2.
KW HYPOTHETICAL PROTEIN; RIBOSOMAL PROTEIN.
SQ SEQUENCE 121 AA; 13641 MW; 9CA08085 CRC32;

Query Match 36.2%; Score 51; DB 11; Length 121;
Best Local Similarity 25.0%; Pred. No. 8.32e+00;
Matches 3; Conservative 8; Mismatches 1; Indels 0; Gaps 0;

Db 78 gsrcancvkeri 89
: :| |::| |
Qy 6 GTKSKRCVRQKV 17

RESULT 23
ID VP67_NPVGM STANDARD; PRT; 337 AA.
AC P04872;
DT 13-AUG-1987 (REL. 05, CREATED)
DT 01-AUG-1990 (REL. 15, LAST SEQUENCE UPDATE)
DT 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
DE MAJOR ENVELOPE GLYCOPROTEIN (GP67) (FRAGMENT).
GN GP67 OR P67.
OS GALLERIA MELLONELLA NUCLEAR POLYHEDROSIS VIRUS (GNPV).
OC VIRIDAE; DS-DNA ENVELOPED VIRUSES; BACULOVIRIDAE; EUBACULOVIRINAE.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 84132566.
RA BLINOV V.M., GUTOV V.V., HOLODILOV N.G., ILJICHEV A.A.,
RA KARGINOV V.A., MIKRUKOV N.N., MORDEVINOV V.A., NIKONOV I.V.,
RA PETROV N.A., URMANOV I.H., VASILENKO S.K.;
RL FEBS LETT. 167:254-258(1984).
CC -1- FUNCTION: PHOSPHOGLYCOPROTEIN WHICH IS LOCATED ON THE SURFACE OF
CC BOTH INFECTED CELLS AND BUDDING VIRIONS. IT IS SUGGESTED THAT THE
CC VIRUS ENTRY INTO CELLS IS PRIMARILY BY THE ENDOCYTIC PATHWAY AND
CC THAT THIS PROTEIN MAY PLAY A ROLE IN FUSION OF THE VIRAL ENVELOPE
CC WITH THE ENDOSONAL MEMBRANE.
CC -1- PTM: ACYLATED BY A PALMITIC ACID GROUP.
CC -1- SIMILARITY: TO THE CORRESPONDING PROTEIN IN OTHER BACULOVIRUSES;
CC ALSO SOME SIMILARITY TO DHORI AND THOGOTO VIRUSES MAJOR ENVELOPE
CC GLYCOPROTEIN.
CC -1- CAUTION: THIS IS A CONCEPTUAL TRANSLATION; THIS SEQUENCE WAS
CC TRANSLATED USING THE ACMPV SEQUENCE AS A TEMPLATE. THERE IS A

```

CC' FRAMESHIFT IN THE ORIGINAL NUCLEOTIDE SEQUENCE.
 DR EMBL; X00410; G58675; ALT_FRAME.
 DR PIR; S07237; S07237.

KW GLYCOPROTEIN; TRANSMEMBRANE; PHOSPHORYLATION; LIPOPROTEIN.
 FT NON_TER 1 1
 FT CARBOHYD 76 76 POTENTIAL.
 FT CARBOHYD 114 114 POTENTIAL.
 FT CARBOHYD 271 271 POTENTIAL.
 FT CARBOHYD 301 301 POTENTIAL.
 FT NON_TER 337 337
 SQ SEQUENCE 337 AA; 39000 MW; 3772A3FA CRC32;

Query Match 36.2%; Score 51; DB 10; Length 337;
 Best Local Similarity 45.5%; Pred. No. 8.32e+00;
 Matches 5; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Db 180 kfncdkrkve 190
 QY 8 KSKCVQKVE 18
 | : : : : | | | |

RESULT 24
 ID ADH1_ZYMO STANDARD; PRT; 337 AA.
 AC P20368;
 DT 01-FEB-1991 (REL. 17, CREATED)
 DT 01-FEB-1991 (REL. 17, LAST SEQUENCE UPDATE)
 DT 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
 DE ALCOHOL DEHYDROGENASE I (EC 1.1.1.1) (ADH 1).
 GN ADHA.
 OS ZYMONAS MOBILIS.
 OC PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;
 OC UNCERTAIN.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CP4;
 RX MEDLINE; 90236908.
 RA KESHAV K.F., YOMANO L.P., AN H., INGRAM L.O.;
 RL J. BACTERIOL. 172:2491-2497(1990).
 RN [2]
 RP SEQUENCE OF 1-40 FROM N.A.
 RC STRAIN-CP4;
 RX MEDLINE; 93308069.
 RA YOMANO L.P., SCOPES R.K., INGRAM L.O.;
 RL J. BACTERIOL. 175:3926-3933(1993).
 RN [3]
 RP SEQUENCE OF 1-31.
 RX MEDLINE; 86108298.
 RA NEALE A.D., SCOPES R.K., KELLY J.M., WETTENHALL R.E.H.;
 RL EUR. J. BIOCHEM. 154:119-124(1986).
 CC -1- CATALYTIC ACTIVITY: ALCOHOL + NAD(+) - ALDEHYDE OR KETONE + NADH.
 CC -1- PATHWAY: ETHANOGENIC.
 CC -1- ENZYME REGULATION: ADHA IS INHIBITED BY ETHANOL.
 CC -1- COFACTOR: REQUIRES ZINC FOR ITS ACTIVITY.
 CC -1- SUBUNIT: MULTIMERIC (WITH DIFFERENT RATIOS OF MONOMERS).
 CC -1- IN Z. MOBILIS THERE ARE TWO ISOZYMES OF ALCOHOL DEHYDROGENASE.
 CC -1- SIMILARITY: BELONGS TO THE ZINC ALCOHOL DEHYDROGENASES.

DR EMBL; M32100; G155571; -.
 DR EMBL; L09650; E84191; -.
 DR PIR; A35260; A35260.
 DR PIR; A24801; A24801.
 DR HSP; P00325; 1HDH.
 DR PROSITE; PS0059; ADH_ZINC.
 KW OXIDOREDUCTASE; ZINC; NAD.
 FT METAL 37 37
 FT METAL 58 58 ZINC (CATALYTIC) (BY SIMILARITY).
 FT METAL 89 89 ZINC (CATALYTIC) (BY SIMILARITY).
 FT METAL 92 92 ZINC (SECOND ATOM) (BY SIMILARITY).
 FT METAL 95 95 ZINC (SECOND ATOM) (BY SIMILARITY).
 FT METAL 103 103 ZINC (SECOND ATOM) (BY SIMILARITY).
 FT METAL 145 145 ZINC (CATALYTIC) (BY SIMILARITY).
 FT METAL 17 17 T -> I (IN REF. 3).
 FT CONFLICT 26 26 E -> F (IN REF. 3).
 FT CONFLICT 28 28 L -> H (IN REF. 3).

FT CONFLICT 30 30 E -> P (IN REF. 3).
 SQ SEQUENCE 337 AA; 36094 MW; 7B77AE15 CRC32;
 Query Match 36.2%; Score 51; DB 1; Length 337;
 Best Local Similarity 30.0%; Pred. No. 8.32e+00;
 Matches 6; Conservative 7; Mismatches 7; Indels 0; Gaps 0;
 Db 210 vinpknedaaakikekvga 229
 QY 1 VIDHQGTSKSKVQRKVEGS 20
 | : : : : | : : : : |

RESULT 25
 ID KPY1_ECOLI STANDARD; PRT; 462 AA.
 AC P14178;
 DT 01-JAN-1990 (REL. 13, CREATED)
 DT 01-JAN-1990 (REL. 13, LAST SEQUENCE UPDATE)
 DT 01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)
 DE PYRUVATE KINASE I (EC 2.7.1.40) (PK-1).
 GN PYKF.
 OS ESCHERICHIA COLI.
 OC PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;
 OC ENTEROBACTERIACEAE.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 89386643.
 RA OHARA O., DORIT R.L., GILBERT W.;
 RL PROC. NATL. ACAD. SCI. U.S.A. 86:6883-6887(1989).
 RN [2]
 RP SEQUENCE OF 293-319; 369-385 AND 389-404.
 RX MEDLINE; 89228557.
 RA SPERANZA M.L., VALENTINI G., IADAROLA P., STOPPINI M., MALCOVATI M.,
 RA FERRI G.;
 RL BIOL. CHEM. HOPPE-SEYLER 370:211-216(1989).
 RN [3]
 RP SEQUENCE OF 1-48.
 RX MEDLINE; 91315755.
 RA VALENTINI G., STOPPINI M., SPERANZA M.L., MALCOVATI M., FERRI G.;
 RL BIOL. CHEM. HOPPE-SEYLER 372:91-93(1991).
 RN [4]
 RP SEQUENCE OF 1-12.
 RC STRAIN-K12 / EMG2;
 LINK A.J.;
 RL SUBMITTED (OCT-1994) TO THE SWISS-PROT DATA BANK.

CC -1- CATALYTIC ACTIVITY: ATP + PYRUVATE -> ADP + PHOSPHOENOLPYRUVATE.
 CC -1- SUBUNIT: HOMOTETRAMER.
 CC -1- COFACTOR: REQUIRES MAGNESIUM AND POTASSIUM.
 CC -1- PATHWAY: FINAL STEP IN GLYCOLYSIS.
 CC -1- ENZYME REGULATION: BELONGS TO TYPE I PK; FRUCTOSE
 1,6-BISPHOSPHATE-ACTIVATED.
 CC -1- SIMILARITY: HIGH, WITH OTHER PYRUVATE KINASES.
 DR EMBL; M24636; G147276; -.
 DR PIR; S03397; S03397.
 DR PIR; S13434; S13434.
 DR PIR; S29004; S29004.
 DR HSP; P11974; 1PKN.
 DR EC02DBASE; G054.7; 6TH EDITION.
 DR ECOGENE; EG10804; PYKF.
 DR PROSITE; PS00110; PYRUVATE_KINASE.
 KW TRANSFERASE; KINASE; GLYCOLYSIS; MULTIGENE FAMILY; MAGNESIUM.
 FT ACT_SITE 220 220 BY SIMILARITY.
 FT METAL 222 222 MAGNESIUM (BY SIMILARITY).
 FT METAL 243 243 MAGNESIUM (BY SIMILARITY).
 FT METAL 244 244 MAGNESIUM (BY SIMILARITY).
 FT CONFLICT 44 44 G -> S (IN REF. 3).
 FT CONFLICT 379 379 Q -> N (IN REF. 2).
 FT CONFLICT 401 401 T -> D (IN REF. 2).
 SQ SEQUENCE 462 AA; 50308 MW; D83D4CE0 CRC32;

Query Match 36.2%; Score 51; DB 5; Length 462;
 Best Local Similarity 50.0%; Pred. No. 8.32e+00;
 Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Db 375 vvatgggksaravr 388
|: || ||: ||
Qy 1 VIDHQGTKSSKCVR 14

Search completed: Tue Jul 29 07:31:16 1997
Job time : 17 secs.

M P S R C H

(TM)

Release 2.1D John F. Collins, Biocomputing Research Unit.
Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K.
Distribution rights by IntelliGenetics, Inc.

MPSrch_pp protein - protein database search, using Smith-Waterman algorithm
Run on: Tue Jul 29 07:32:27 1997; MasPar time 2.20 Seconds
Tabular output not generated. 104.214 Million cell updates/sec

Title: >US-08-487-283A-1
Description: (1-21) from US08487283A.pep
Perfect Score: 141
Sequence: 1 VIDHGRKSSKCVQRKVEGSS 21

Scoring table: PAM 150
Gap 15

Searched: 92623 seqs, 10896596 residues

Post-processing: Minimum Match 0%
Listing first 100 summaries

Database: a-geneseq26
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19

Statistics: Mean 18.695; Variance 55.381; scale 0.338

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES						
Result No.	Score	Query Match %	Length	ID	Description	Pred. No.
1	141	100.0	21	15	R77605 Pro-C5 polypeptide KS	8.75e-10
2	141	100.0	1676	15	R77604 Pro-C5 polypeptide.	8.75e-10
3	55	39.0	264	4	R22271 CShase.	2.91e+01
4	54	38.3	1732	17	R96029 P. gingivalis porphyrin	3.72e+01
5	54	38.3	3163	16	R94347 Hepatitis GB virus (H	3.72e+01
6	53	37.6	589	3	R14327 Mouse epithelin precu	4.75e+01
7	53	37.6	652	15	R88124 Tobacco mosaic virus	4.75e+01
8	53	37.6	1009	5	R26206 Type B human platelet	4.75e+01
9	53	37.6	1089	2	R06910 Alpha type PDGF recep	4.75e+01
10	53	37.6	1089	2	R08287 Platelet derived grow	4.75e+01
11	53	37.6	1196	19	W04326 Rat petrin.	4.75e+01
12	52	36.9	354	6	R33439 Ornithine cyclodeamin	6.06e+01
13	51	36.2	589	3	R14325 Rat epithelin precurs	7.71e+01
14	51	36.2	914	3	R15785 B.thuringiensis toxin	7.71e+01
15	51	36.2	956	3	R15784 B.thuringiensis toxin	7.71e+01
16	51	36.2	986	9	R25141 B.thuringiensis toxin	7.71e+01
17	51	36.2	1100	3	R15783 B.thuringiensis toxin	7.71e+01
18	51	36.2	1129	13	R70830 Murine JAK2 kinase.	7.71e+01
19	51	36.2	1144	15	R88123 Tobacco mosaic virus	7.71e+01
20	51	36.2	1144	15	R88122 Tobacco mosaic virus	7.71e+01

21	51	36.2	1588	9	R46605 Malarial PfEMP3 epit	7.71e-01
22	51	36.2	1663	9	R46608 Plasmodium falciparum	7.71e-01
23	49	34.8	429	10	R50036 Hantaan virus Nucleo	1.24e-02
24	49	34.8	487	3	R13794 Drosophila hormone re	1.24e-02
25	49	34.8	594	1	R04107 DNA-binding protein G	1.24e-02
26	49	34.8	1323	10	R55248 N-methyl-D-aspartic a	1.24e-02
27	49	34.8	1336	12	R66041 Human N-methyl-D-aspa	1.24e-02
28	49	34.8	3080	1	P93285 Sequence of clone HIV	1.24e-02
29	48	34.0	399	19	W04218 Human urinary bladder	1.58e-02
30	48	34.0	925	14	R79148 Human insulin recepto	1.58e-02
31	48	34.0	1299	15	R86304 Drosophila patched pr	1.58e-02
32	47	33.3	122	16	R81443 Hepatitis GB virus (H	1.99e-02
33	47	33.3	458	3	R15149 CD4 coordinate system	1.99e-02
34	47	33.3	498	3	R12255 HIV-1 strain OVI GAG	1.99e-02
35	47	33.3	792	16	R85198 Avenacinase - a sapon	1.99e-02
36	47	33.3	793	16	R85200 Avenacinase-like prot	1.99e-02
37	47	33.3	793	16	R85199 Avenacinase-like prot	1.99e-02
38	47	33.3	2873	17	R87559 Hepatitis virus clone	1.99e-02
39	47	33.3	2873	18	R90796 HGV-PNF 2161 polyprot	1.99e-02
40	46	32.6	376	5	R25429 Cellulase contained i	2.51e-02
41	46	32.6	376	7	R37151 Dye transfer inhibiti	2.51e-02
42	46	32.6	376	5	R27969 Endoglucanase enzyme.	2.51e-02
43	46	32.6	376	5	R25527 Fusarium oxysporum DS	2.51e-02
44	46	32.6	376	3	R15272 Fusarium oxysporum DS	2.51e-02
45	46	32.6	376	5	R25466 Endoglucanase #2.	2.51e-02
46	46	32.6	376	8	R42064 Endoglucanase enzyme.	2.51e-02
47	46	32.6	1087	17	R96028 P. gingivalis haemag	2.51e-02
48	46	32.6	1232	19	R98217 Neuronal apoptosis in	2.51e-02
49	46	32.6	1358	17	R96032 P. gingivalis haemag	2.51e-02
50	46	32.6	1687	17	R96033 P. gingivalis haemag	2.51e-02
51	46	32.6	1704	13	R70188 Arg-gingipain-2 prepo	2.51e-02
52	45	31.9	33	16	R82896 Human B7-1 signal pep	3.16e-02
53	45	31.9	51	8	R38884 lac peptide fragment.	3.16e-02
54	45	31.9	170	3	R10845 Feline interferon fro	3.16e-02
55	45	31.9	171	1	P90398 Feline interferon	3.16e-02
56	45	31.9	194	1	P90399 Feline interferon	3.16e-02
57	45	31.9	288	13	R67989 Human B lymphocyte an	3.16e-02
58	45	31.9	312	4	R21848 Sequence of Plasmodiu	3.16e-02
59	45	31.9	360	16	R85552 Mutant lactose repres	3.16e-02
60	45	31.9	360	8	R40926 Wild-type lacI.	3.16e-02
61	45	31.9	370	8	R40927 CpG depleted lacI gen	3.16e-02
62	45	31.9	386	12	R60549 Murine developmental	3.16e-02
63	45	31.9	505	14	R77172 Condensing enzyme clo	3.16e-02
64	45	31.9	605	14	R74186 Chick p78.	3.16e-02
65	45	31.9	709	1	P91934 B1 antigen.	3.16e-02
66	45	31.9	845	13	R70065 Hepatitis B virus pol	3.16e-02
67	45	31.9	850	11	R60546 Mature murine develop	3.16e-02
68	45	31.9	868	2	R07454 Second open reading f	3.16e-02
69	45	31.9	874	11	R60545 Murine developmental	3.16e-02
70	45	31.9	880	13	R77846 Mouse Rse rPRK.	3.16e-02
71	45	31.9	1277	10	R52701 Plasmid pASK60-Strep	3.16e-02
72	45	31.9	2324	1	R05707 Acetyl-CoA-carboxylas	3.16e-02
73	45	31.9	2910	17	R87566 Hepatitis G virus clo	3.16e-02
74	45	31.9	2910	18	R90797 HGV-JC variant polypr	3.16e-02
75	45	31.9	2938	11	R59223 GAP protein Irai.	3.16e-02
76	45	31.9	3011	16	R95020 Hepatitis GB virus (H	3.16e-02
77	44	31.2	15	1	P90197 Antigenic peptide for	3.97e-02
78	44	31.2	20	12	R68766 Cytotoxic T lymphocyt	3.97e-02
79	44	31.2	23	1	P80572 Peptide region of hum	3.97e-02
80	44	31.2	25	12	R68764 Cytotoxic T lymphocyt	3.97e-02
81	44	31.2	35	12	R63489 Human MTR77 serotonin	3.97e-02
82	44	31.2	130	1	P91387 HIV LTR sequence	3.97e-02
83	44	31.2	130	10	R56876 N-terminal fragment e	3.97e-02
84	44	31.2	168	10	R55858 HIV-1 MA delta-116-12	3.97e-02
85	44	31.2	355	7	R38297 dTDP-D-glucose syntha	3.97e-02
86	44	31.2	422	11	R58599 Fowlpox virus protein	3.97e-02
87	44	31.2	500	2	P70269 The sequence encoding	3.97e-02
88	44	31.2	504	4	P93707 Sequence of the gag p	3.97e-02
89	44	31.2	508	2	P70666 Sequence encoded by L	3.97e-02
90	44	31.2	512	8	R43866 HTLV-III GAG gene pro	3.97e-02
91	44	31.2	515	1	P91235 (ENV-80)(GAG-VII) hex	3.97e-02
92	44	31.2	528	13	R73006 Aminopeptidase O12 cl	3.97e-02
93	44	31.2	529	14	R74188 Mouse p78.	3.97e-02

94 44 31.2 533 3 R15057 Cytochrome P450C25. 3.97e+02
 95 44 31.2 600 2 P70541 HTLV-III gag/env gene 3.97e+02
 96 44 31.2 600 2 P70544 Sequence of HTLV-III 3.97e+02
 97 44 31.2 741 1 P80136 Neisseria IgA-Proteas 3.97e+02
 98 44 31.2 1025 8 R38863 GC-B. Natriuretic Pep 3.97e+02
 99 44 31.2 1047 3 R10399 Human Natriuretic Pep 3.97e+02
 100 44 31.2 1047 3 R10867 NPRB(Pro655, Glu656, 3.97e+02

ALIGNMENTS

RESULT 1
 ID R77605 standard; Protein; 21 AA.
 AC R77605;
 DT 02-APR-1996 (first entry)
 DE Pro-C5 polypeptide KSSKC epitope.
 KW Complement C5; haemolysis; kidney; glomerulonephritis;
 KW monoclonal antibody; antiinflammatory; antibody engineering;
 KW humanised antibody; KSSKC epitope.
 OS Homo sapiens.
 PN W09529697-A1.
 PD 09-NOV-1995.
 PF 01-MAY-1995; U05688.
 PR 02-MAY-1994; US-236208.
 PA (ALEX-) ALEXION PHARM INC.
 PI Evans MJ, Matis L, Mueller EE, Nye SH, Rollins S;
 PI Rother RP, Springhorn J P, Squinto SP, Thomas TC;
 PI Wang Y, Wilkins JA;
 DR WPI: 95-392923/50.
 DT Treating glomerulonephritis with antibody against complement C5
 PT component - to inhibit complement induced cell lysis
 PS Example 13; Page 82-92; 181pp; English.
 CC The cDNA sequence of the complement C5 gene transcript predicts a
 CC secreted pro-C5 precursor of 1676 amino acids (R77604). C5 is a
 CC beta-globulin heterodimer thought to play a role in the pathogenesis
 CC of glomerulonephritis (GN). Cleavage of the C5 alpha-chain
 CC by a convertase enzyme generates anaphylatoxic C5a. Monoclonal
 CC and humanised recombinant antibodies that recognise the alpha-chain
 CC KSSKC epitope (R77605) block C5a generation, thereby reducing
 CC glomerular inflammation and kidney dysfunction associated with GN.
 SQ Sequence 21 AA;

Query Match 100.0%; Score 141; DB 15; Length 21;
 Best Local Similarity 100.0%; Pred. No. 8.75e-10;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 vidhgktskcvrkqvegss 21
 |||||
 QY 1 VIDHGTSSKCVRKQVEGSS 21

RESULT 2
 ID R77604 standard; Protein; 1676 AA.
 AC R77604;
 DT 15-MAR-1996 (first entry)
 DE Pro-C5 polypeptide.
 KW Complement C5; haemolysis; kidney; glomerulonephritis;
 KW monoclonal antibody; antiinflammatory; antibody engineering;
 KW humanised antibody.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT Peptide 1..18
 FT /label= Sig_peptide
 FT Protein 19..673
 FT /label= Beta-chain
 FT Cleavage_site 673..674
 FT Cleavage_site 677..678
 FT Peptide 674..677
 FT label= Cleavage_peptide
 FT Protein 678..1676
 FT /label= Alpha-chain
 FT /note= "amino acids 872-892 (854-874 of
 the mature protein) comprise the KSSKS

FT epitope*
 FT Peptide 678..751
 FT /label= C5a
 FT Cleavage_site 751..752
 FT /label= Convertase_cleavage_site
 FT Modified_site 911
 FT /label= N-glycosylation_site
 FT Modified_site 1115
 FT /label= N-glycosylation_site
 FT Modified_site 1630
 FT /label= N-glycosylation_site
 PN W09529697-A1.
 PD 09-NOV-1995.
 PF 01-MAY-1995; U05688.
 PR 02-MAY-1994; US-236208.
 PA (ALEX-) ALEXION PHARM INC.
 PI Evans MJ, Matis L, Mueller EE, Nye SH, Rollins S;
 PI Rother RP, Springhorn J P, Squinto SP, Thomas TC;
 PI Wang Y, Wilkins JA;
 DR WPI: 95-392923/50.
 DT Treating glomerulonephritis with antibody against complement C5
 PT component - to inhibit complement induced cell lysis
 PS Example 13; Page 82-92; 181pp; English.
 CC The cDNA sequence of the complement C5 gene transcript predicts a
 CC secreted pro-C5 precursor of 1676 amino acids (R77604). C5 is a
 CC beta-globulin heterodimer thought to play a role in the pathogenesis
 CC of glomerulonephritis (GN). Cleavage of the C5 alpha-chain
 CC by a convertase enzyme generates anaphylatoxic C5a. Monoclonal
 CC and humanised recombinant antibodies that recognise the alpha-chain
 CC KSSKC epitope (R77605) block C5a generation, thereby reducing
 CC glomerular inflammation and kidney dysfunction associated with GN.
 SQ Sequence 1676 AA;

Query Match 100.0%; Score 141; DB 15; Length 1676;
 Best Local Similarity 100.0%; Pred. No. 8.75e-10;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 872 vidhgktskcvrkqvegss 892
 |||||
 QY 1 VIDHGTSSKCVRKQVEGSS 21

RESULT 3
 ID R22271 standard; Protein; 264 AA.
 AC R22271;
 DT 30-JUL-1992 (first entry)
 DE CSHase.
 KW N-carbamoyl-sarcosine amidohydrolase; CSH; assay; diagnosis;
 KW creatinine.
 OS Arthrobacter sp. DSM 2563.
 PN EP-476670-A.
 PD 25-MAR-1992.
 PF 19-SEP-1991; 115974.
 PR 20-SEP-1990; DE-029844.
 PA (BOEF) BOEHRINGER MANNHEIM GMBH.
 PI Bartscher H, Schumacher G;
 DR WPI: 92-098378/13.
 DR N-PSDB; Q22713.
 DT Recombinant DNA encoding N-carbamoyl-sarcosine-amidohydrolase -
 PT useful in clinical assay of creatinine, and vectors providing
 PT efficient expression in E.coli
 PS Claim 9; Page 9 + 7; 12pp; German.
 CC The sequence encoding CSHase is useful in assay of creatinine
 CC (for diagnosis of kidney disease). It can now be prepd. more
 CC simply than by known methods which involve culture of Arthrobacter
 CC on complex media.
 SQ Sequence 264 AA;

Query Match 39.0%; Score 55; DB 4; Length 264;
 Best Local Similarity 46.2%; Pred. No. 2.91e+01;
 Matches 6; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
 Db 171 gataagcvrhtve 183

FT /label= EP
 FT /note= "claim 28, page 56"
 PN WO9115510-A.
 PD 17-OCT-1991.
 PF 03-APR-1991; U02321.
 PR 03-APR-1990; US-504508.
 PR 13-MAR-1991; US-083796.
 PA (BRIM) BRISTOL-MYERS SQUIB.
 PI Shoyab M, Plowman GD;
 DR WPI; 91-325168/44.
 DR N-PSDB; Q14340.
 PT New cysteine-rich growth modulating proteins, epithelins - useful
 PT as inhibitors of neoplastic cell growth and to promote wound
 PT healing and treat psoriasis
 PS Disclosure; Fig 23; 97pp; English.
 CC ET-1 is a bifunctional growth regulator, capable of stimulating
 CC the growth of some cell types while inhibiting the growth of others.
 CC ET-2 is functionally similar to ET-1 w.r.t. growth inhibitory
 CC bioactivity. In contrast, however, ET-2 is apparently not capable of
 CC eliciting the growth stimulatory activity characteristic of ET-1 and,
 CC in fact, antagonises this ET-1 activity.
 CC See also Q14338-40, Q14952-53, R14328-9 and R15315-20.
 SQ Sequence 589 AA;

Query Match 37.6%; Score 53; DB 3; Length 589;
 Best Local Similarity 35.7%; Pred. No. 4.75e+01;
 Matches 5; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

Db 560 hcsargtkclrkki 573

QY 4 HQGTRKSKVRQKV 17
 | : : : : | : : | :
 | : : : : | : : | :

RESULT 7

ID R88124 standard; Protein; 652 AA.
 AC R88124;
 DT 28-MAR-1996 (first entry)
 DE Tobacco mosaic virus resistance N gene truncated protein.
 KW Tobacco mosaic virus resistance; TMV; N gene; Solanaceae;
 KW crop improvement; transgenic plant; crop improvement.
 OS Nicotiana glutinosa.
 PN WO9535024-A1.
 PD 28-DEC-1995.
 PF 16-JUN-1995; U07754.
 PR 17-JUN-1994; US-261663.
 PA (REGC) UNIV CALIFORNIA.
 PA (USDA) US SEC OF AGRIC.
 PI Baker BJ, Whitham SA;
 DR WPI; 96-058144/06.
 DR N-PSDB; T09342.
 PT Plant virus resistance gene N sequences from tobacco - useful for
 PT generating transgenic Solanaceous plants resistant to Tobacco Mosaic
 PT Virus
 PS Claim 28; Page 75-79; 98pp; English.
 CC The Nicotiana glutinosa N gene truncated protein (R88124) mediates
 CC resistance to tobacco mosaic virus (TMV). A cDNA clone (T09342)
 CC coding for the protein was obt'd. from a N. glutinosa leaf cDNA
 CC library by transposon tagging. DNA sequences encoding the
 CC protein can be used to generate transgenic plants, esp. Solanaceae,
 CC resistant to TMV.
 SQ Sequence 652 AA;

Query Match 37.6%; Score 53; DB 15; Length 652;
 Best Local Similarity 31.3%; Pred. No. 4.75e+01;
 Matches 5; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

Db 156 dnrdktadacirgvd 171

QY 3 HHQGTKSKVRQKVE 18
 | : : | : | : | :
 | : : | : | : | :

RESULT 8

ID R26206 standard; Protein; 1009 AA.

AC R26206;
 DT 09-FEB-1993 (first entry)
 DE Type B human platelet-derived growth factor receptor.
 KW PDGF; PDGF-R; mesenchyme; tyrosine kinase; ligand binding region.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT Peptide 1..23
 FT /label= Signal_peptide
 FT Protein 24..1009
 FT /label= Mature_PDGf-A
 PN WO9213867-A.
 PD 20-AUG-1992.
 PF 28-JAN-1992; U00730.
 PR 31-JAN-1991; US-650793.
 PA (CORP-) COR THERAPEUTICS INC.
 PI Escobedo JA, Fretto LJ, Giese NA, Tomlinson JE, Williams LT;
 PI Wolf D;
 DR WPI; 92-299970/36.
 DR N-PSDB; Q27451.
 PT Platelet derived growth factor receptor (PDGF-R) poly:peptide(s)
 PT - useful as therapeutic and diagnostic agents e.g. for assaying
 PT PDGF activity in sample
 PS Disclosure; Page 90; 109pp; English.
 CC The sequence given is one allele of type A human platelet-derived
 CC growth factor (PDGF) receptor (PDGF-R). This receptor is typically
 CC found on cells of mesenchymal origin. It acts while in the form of
 CC two transmembrane glycoproteins, each of which is about 180 kD.
 CC This receptor has three major regions. The first is a transmembrane
 CC region, which spans the membrane once, separating the regions of the
 CC receptor exterior to the cell from those interior to the cell. The
 CC second region is an extracellular region which contains the domains
 CC which bind the PDGF. The third region is an intracellular region
 CC which possesses a tyrosine kinase activity. This tyrosine kinase
 CC domain is notable in having an insert of approx. 100 amino acids,
 CC as compared with most other receptor tyrosine kinase domains which
 CC are contiguous or have shorter insert sequences. Fragments of this
 CC sequence between 8 and 400 amino acids comprising one or more PDGF
 CC ligand binding region from the extracellular domain may be used to
 CC bind a PDGF ligand.
 SQ Sequence 1009 AA;

Query Match 37.6%; Score 53; DB 5; Length 1009;
 Best Local Similarity 38.1%; Pred. No. 4.75e+01;

Matches 8; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

Db 381 vddhgstggtvtrctaeftp 401

QY 1 VIDHQGTKSKVRQKVEGSS 21
 | : : : : | : : | : :
 | : : : : | : : | : :

RESULT 9

ID R06910 standard; protein; 1089 AA.
 AC R06910;
 DT 16-JAN-1991 (first entry)
 DE Alpha type PDGF receptor deduced from TR4 cDNA clone.
 KW Platelet derived growth factor; Tll.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT Domain 1..23
 FT /label=signal peptide
 FT Domain 24..524
 FT /label=ligand binding domain
 FT Domain 525..548
 FT /label=transmembrane region
 FT Domain 549..599
 FT /label=juxtamembrane domain
 FT Binding-site 600..627
 FT /label=Arp binding site
 FT Modified-site 849
 FT /label=tyrosine autophosphorylation site
 FT Modified-site 42..44
 FT /label=N-glycos_site
 FT Modified-site 76..78

FT /label-N-glycos_site
FT Modified-site 103..105
FT /label-N-glycos_site
FT Modified-site 179..181
FT /label-N-glycos_site
FT Modified-site 353..355
FT /label-N-glycos_site
FT Modified-site 359..361
FT /label-N-glycos_site
FT Modified-site 458..460
FT /label-N-glycos_site
FT Modified-site 468..470
FT /label-N-glycos_site
FT W09010013-A.
PD 07-SEP-1990.
PD 08-FEB-1989; US-308282.
PR (USDC) US SEC OF COMMERCE.
PA Matsui T, Aaronson SA, Pierce JH;
PI WPI; 90-290306/38.
DR N-PSDB: Q05989.
DR N-PSDB: Q05989.
PT Type alpha platelet-derived growth factor receptor gene - useful
PT for transforming cells to express novel protein receptor and also
PT susceptible to genetic engineering.
PS Claim 7; Fig 3; 64pp; English.
CC The TR4 clone is the largest cDNA clone related to the T11 genomic
CC clone isolated from a library prepd. from human thymus DNA. The
CC T4 cDNA clone was isolated from a M426 human embryo fibroblast
CC cDNA library. The coding region can be introduced into the pSV2
CC gpt vector with a simian sarcoma virus LTR as a promoter and
CC expressed in a host. The resulting protein is a novel PDGF
CC receptor designated type alpha (the known receptor is designated
CC type beta). The polypeptide has a calculated molecular mass of 120
CC kD and has all the characteristics of a membrane spanning tyrosine
CC kinase receptor. The extracellular region comprises a hydrophobic
CC signal peptide and a ligand binding domain which has structural
CC homology with the PDGF-R/CSP1-R subfamily. Ten Cys residues are
CC spaced at the same positions as in other receptors of the sub-
CC family and eight potential N-linked glycosylation sites are also
CC present. A hydrophobic segment spans the membrane and the cyto-
CC plasmic region comprises a juxtamembrane region, a tyrosine kinase
CC region split into TK1 and TK2 by a hydrophilic interkinase region
CC and a hydrophilic C-terminal tail. The TK region includes the
CC consensus ATP binding sequence (G-X-G-X-X-G...K) and a tyrosine
CC autophosphorylation site homologous to that of pp60(v-src).
SQ Sequence 1089 AA;
Query Match 37.6%; Score 53; DB 2; Length 1089;
Best Local Similarity 38.1%; Pred. No. 4.75e+01;
Matches 8; Conservative 6; Mismatches 7; Indels 0; Gaps 0;
Db 421 vddhgstgggtvrcvtaegtp 441
QY 1 VIDHGTGKSSKCVKQKVEGSS 21
RESULT 10
ID R08267 standard; protein; 1089 AA.
AC R08267;
DE 07-MAR-1991 (first entry)
DE Platelet derived growth factor (PDGF) receptor protein.
KW Atherosclerosis; fibrotic diseases.
OS Homo sapiens.
PN W09014425-A.
PD 29-NOV-1990.
PD 21-MAY-1989; U02849.
PR 22-MAY-1989; US-355018.
PA (ZYMO-) ZYMOGENETICS INC.
PI Kelly JD, Murray MJ;
PI WPI; 90-375992/50.
DR N-PSDB: Q06869.
PT DNA encoding platelet-derived growth factor - used to transform
PT cells for culturing to detect PDG agonists and antagonists

PS Claim 1; Fig 1; 30pp; English.
CC Gene product may be expressed from a transformed cell. It has
CC utility in dection of PDGF agonist and antagonist analogues, binding
CC AA, AB and BB isoforms. PDGF agonists may be used to enhance wound
CC healing, and antagonists may be used to block the effects of PDGF
CC eg. in treatment of atherosclerosis or fibrotic diseases.
SQ Sequence 1089 AA;
Query Match 37.6%; Score 53; DB 2; Length 1089;
Best Local Similarity 38.1%; Pred. No. 4.75e+01;
Matches 8; Conservative 6; Mismatches 7; Indels 0; Gaps 0;
Db 421 vddhgstgggtvrcvtaegtp 441
QY 1 VIDHGTGKSSKCVKQKVEGSS 21
RESULT 11
ID W04326 standard; Protein; 1196 AA.
AC W04326;
DE 16-JAN-1997 (first entry)
DE Rat petrin.
KW Petrin; neurite outgrowth associated protein; CNS;
KW central nervous system; myelin; protein phosphatase 2C; stroke;
KW neurodegeneration.
OS Rattus sp.
FT Key Location/Qualifiers
FT Misc_difference 129
FT /note= "corresponds to stop codon in DNA sequence"
FT Misc_difference 192
FT /note= "corresponds to stop codon in DNA sequence"
FT Misc_difference 205
FT /note= "corresponds to stop codon in DNA sequence"
FT Misc_difference 219
FT /note= "corresponds to stop codon in DNA sequence"
FT Misc_difference 225
FT /note= "corresponds to stop codon in DNA sequence"
FT Misc_difference 234
FT /note= "corresponds to stop codon in DNA sequence"
FT Misc_difference 243
FT /note= "corresponds to stop codon in DNA sequence"
FT Misc_difference 269
FT /note= "corresponds to stop codon in DNA sequence"
FT Misc_difference 285
FT /note= "corresponds to stop codon in DNA sequence"
FT Misc_difference 312
FT /note= "corresponds to stop codon in DNA sequence"
FT Misc_difference 319
FT /note= "corresponds to stop codon in DNA sequence"
FT Misc_difference 344
FT /note= "corresponds to stop codon in DNA sequence"
FT Misc_difference 358
FT /note= "corresponds to stop codon in DNA sequence"
FT Misc_difference 378
FT /note= "corresponds to stop codon in DNA sequence"
FT Misc_difference 386
FT /note= "corresponds to stop codon in DNA sequence"
FT Misc_difference 465
FT /note= "corresponds to stop codon in DNA sequence"
FT Misc_difference 473
FT /note= "corresponds to stop codon in DNA sequence"
FT Misc_difference 473
FT /note= "corresponds to stop codon in DNA sequence"
FT Misc_difference 494
FT /note= "corresponds to stop codon in DNA sequence"
FT Misc_difference 555
FT /note= "corresponds to stop codon in DNA sequence"
FT Misc_difference 593
FT /note= "corresponds to stop codon in DNA sequence"
FT Misc_difference 602
FT /note= "corresponds to stop codon in DNA sequence"
FT Misc_difference 609
FT /note= "corresponds to stop codon in DNA sequence"

FT Misc_difference 621 to stop codon in DNA sequence"
 FT /note= "corresponds 724 to stop codon in DNA sequence"
 FT /note= "corresponds 736 to stop codon in DNA sequence"
 FT /note= "corresponds 739 to stop codon in DNA sequence"
 FT /note= "corresponds 786 to stop codon in DNA sequence"
 FT /note= "corresponds 841 to stop codon in DNA sequence"
 FT /note= "corresponds 924 to stop codon in DNA sequence"
 FT /note= "corresponds 934 to stop codon in DNA sequence"
 FT /note= "corresponds 1017 to stop codon in DNA sequence"
 FT /note= "corresponds 1054 to stop codon in DNA sequence"
 FT /note= "corresponds 1127 to stop codon in DNA sequence"
 FT /note= "corresponds 1147 to stop codon in DNA sequence"
 FT /note= "corresponds 1178 to stop codon in DNA sequence"
 FT /note= "corresponds to stop codon in DNA sequence"
 PN WO9632476-A1.
 PD 17-OCT-1996.
 PF 12-APR-1996; CA0214.
 PR 13-APR-1995; US-421701.
 PA (MOUN) MOUNT SINAI HOSPITAL CORP.
 PI Labes M, Lozano A, Roach A, Roder J;
 DR WPI: 96-477127/47.
 DR N-PSDB; T38484.
 PT Assay for substance that modulates response of neuronal cells - and
 PT neurite growth associated protein, Petrin, useful in conditions
 PT involving nerve damage resulting from traumatic injury, stroke or
 PT CNS degenerative disorders
 PS Claim 9; Page 57-61; 119pp; English.
 CC Rat petrin (W04326) is a protein involved in modulating neurite
 CC growth inhibition. The amino sequence was deduced from a cDNA
 CC clone (T38484) derived from an adult rat brain cDNA library; no
 CC coding sequence was indicated. Petrin is a new member of the
 CC protein phosphatase 2C family, and is expressed in neurons in brain
 CC tissue, partic. in the Purkinje cells of the cerebellum. Petrin,
 CC and antibodies raised against it, can be used to modulate neurite
 CC growth and axonal regeneration.
 SQ Sequence 1196 AA;

Query Match 37.6%; Score 53; DB 19; Length 1196;
 Best Local Similarity 61.5%; Pred. No. 4.75e+01;
 Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
 Db 900 vpshtgskphcv 912
 QY 1 VIDHGTSSKCV 13

RESULT 12
 ID R33439 standard; Protein; 354 AA.
 AC R33439;
 DT 06-JUL-1993 (first entry)
 DE Ornithine cyclodeaminase C58 from Ti plasmid pTIC58
 DE mu-crystallins; drug targeting; nervous acting drugs; CNS; neural;
 KW neuronal; neurotransmitter agents; neuromuscular agents; NMJ;
 KW neuromuscular junctions; memory agents; Alzheimers disease;
 KW CNS depressants; CNS stimulants; tranquilisers; muscle relaxants;
 KW antispasmodics; analgesics; anesthetics; anticonvulsants;
 KW antiepileptic agents; antianxiety agents; hallucinogens; sedatives;
 KW hypnotics.
 OS Agrobacterium tumefaciens
 PN US7844304-A.
 PD 01-JAN-1993.

PF 28-FEB-1992; 844304.
 PR 28-FEB-1992; US-844304.
 PA (USSH) US DEPT HEALTH & HUMAN SERVICE.
 PI Kim R, Wistow G;
 DR WPI: 93-093573/11.
 PT New mu-crystalline proteins - having ornithine cyclo-deaminase
 PT activity, used in diagnosis and treatment of disorders in
 PT ornithine metabolism
 PS Disclosure; Page 34; 60pp; English.
 CC This sequence represents ornithine cyclodeaminase (OCD) from
 CC Agrobacterium Ti plasmid pTIC58. It shows approximately 30%
 CC homology with the kangaroo eye lens protein mu-crystallin.
 SQ Sequence 354 AA;

Query Match 36.9%; Score 52; DB 6; Length 354;
 Best Local Similarity 63.6%; Pred. No. 6.06e+01;
 Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Db 312 ryvdrvegss 322
 QY 11 KVRQKVEGSS 21

RESULT 13
 ID R14325 standard; Protein; 589 AA.
 AC R14325;
 DT 17-JAN-1992 (first entry)
 DE Rat epithelin precursor.
 KW ET; growth regulation; inhibition; stimulation.
 OS Rattus rattus.

FT Key Location/Qualifiers
 FT Protein 1..589
 FT /label= precursor
 FT /note= "claim 11, page 54"
 FT Protein 280..335
 FT /label= EP-1
 FT /note= "claim 12, page 54"
 FT Protein 205..261
 FT /label= EP-2
 FT /note= "claim 13, page 54"
 FT Peptide 59..114
 FT /label= EP
 FT /note= "claim 14, page 54"
 FT Peptide 123..179
 FT /label= EP
 FT /note= "claim 15, page 54"
 FT Peptide 362..416
 FT /label= EP
 FT /note= "claim 16, page 54"
 FT Peptide 440..495
 FT /label= EP
 FT /note= "claim 17, page 54"
 FT Peptide 515..570
 FT /label= EP
 FT /note= "claim 18, page 55"
 PN W0911510-A.
 PD 17-OCT-1991.
 PF 03-APR-1991; U02321.
 PR 03-APR-1990; US-504508.
 PR 13-MAR-1991; US-083796.
 PA (BRIM) BRISTOL-MYERS SQUIB.
 PI Shoyab M, Plowman GD;
 DR WPI: 91-325168/44.
 DR N-PSDB; Q14338.

PT New cysteine-rich growth modulating proteins, epithelins - useful
 PT as inhibitors of neoplastic cell growth and to promote wound
 PT healing and treat psoriasis
 PS Disclosure; Fig 18; 97pp; English.
 CC ET-1 is a bifunctional growth regulator, capable of stimulating
 CC the growth of some cell types while inhibiting the growth of others.
 CC ET-2 is functionally similar to ET-1 w.r.t. growth inhibitory
 CC bioactivity. In contrast, however, ET-2 is apparently not capable of
 CC eliciting the growth stimulatory activity characteristic of ET-1 and,

CC in fact, antagonises this ET-1 activity.
 CC See also Q14338-40, Q14952-53, R14328-9 and R15315-20.
 SQ Sequence 589 AA;

Query Match 36.2%; Score 51; DB 3; Length 589;
 Best Local Similarity 46.2%; Pred. No. 7.71e+01;
 Matches 6; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Db 560 hcsakgtklrkk 572

| :|:|:|:|
 Qy 4 HQGKSSKCVQK 16

RESULT 14

ID R15785 standard; Protein; 914 AA.

AC R15785;

DT 10-FEB-1992 (first entry)

DE B.thuringiensis toxin/ACNPV gp64 fusion protein.

KW chimeric; fusion protein; insecticide; ACNPV; Lepidoptera larvae;

OS midgut targeting; bacterial endotoxin; pFAC13.

OS Bacillus thuringiensis var. tenebrionis.

OS Autographa californica Nuclear Polyhedrosis Virus.

PN W09117254-A.

PD 14-NOV-1991.

PF 02-MAY-1991; U03008.

PR 03-MAY-1990; US-518575.

PA (REGC) UNIV OF CALIFORNIA.

PI Sivasubramanian N, Federici A;

DR WPI; 91-353775/48.

DR N-PSDB; Q14807.

PT Extending host range or toxicity of insecticidal proteins - using

protein capable of binding to gut epithelium of insects

PS Claim 55; Fig 18; 61pp; English.

CC A polylinker was inserted into the XmnI restriction site at the

CC carboxyl terminus coding region of B.thuringiensis var. tenebrionis

CC (Btt) toxin. DNA encoding the gp64 viral membrane protein of ACNPV

CC was operably linked to the Btt toxin coding sequence via the

CC polylinker. The gp64 gene sequences act as midgut targeting

CC signals for bacterial endotoxins. Plasmid pFAC13 was one of three

CC different Btt/gp64 gene fusions that were constructed and its

CC deduced amino acid sequence is given here.

CC See also Q14806 and Q14807.

SQ Sequence 914 AA;

Query Match 36.2%; Score 51; DB 3; Length 914;

Best Local Similarity 45.5%; Pred. No. 7.71e+01;

Matches 5; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Db 665 kfncikrkv 675

| :|:|:|:|
 Qy 8 KSSKCVQKVE 18

RESULT 15

ID R15784 standard; Protein; 956 AA.

AC R15784;

DT 10-FEB-1992 (first entry)

DE B.thuringiensis toxin/ACNPV gp64 fusion protein.

KW chimeric; fusion protein; insecticide; ACNPV; Lepidoptera larvae;

OS midgut targeting; bacterial endotoxin; pF7.

OS Bacillus thuringiensis var. tenebrionis.

OS Autographa californica Nuclear Polyhedrosis Virus.

PN W09117254-A.

PD 14-NOV-1991.

PF 02-MAY-1991; U03008.

PR 03-MAY-1990; US-518575.

PA (REGC) UNIV OF CALIFORNIA.

PI Sivasubramanian N, Federici A;

DR WPI; 91-353775/48.

DR N-PSDB; Q14807.

PT Extending host range or toxicity of insecticidal proteins - using

protein capable of binding to gut epithelium of insects

PS Claim 55; Fig 17; 61pp; English.

CC A polylinker was inserted into the XmnI restriction site at the
 CC carboxyl terminus coding region of B.thuringiensis var. tenebrionis
 CC (Btt) toxin. DNA encoding the gp64 viral membrane protein of ACNPV
 CC was operably linked to the Btt toxin coding sequence via the
 CC polylinker. The gp64 gene sequences act as midgut targeting
 CC signals for bacterial endotoxins. Plasmid pF7 was one of three
 CC different Btt/gp64 gene fusions that were constructed and its
 CC deduced amino acid sequence is given here.
 CC See also Q14806 and Q14808.
 SQ Sequence 956 AA;

Query Match 36.2%; Score 51; DB 3; Length 956;

Best Local Similarity 45.5%; Pred. No. 7.71e+01;

Matches 5; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Db 707 kfncikrkv 717

| :|:|:|:|
 Qy 8 KSSKCVQKVE 18

RESULT 16

ID R25141 standard; Protein; 986 AA.

AC R25141;

DT 04-JAN-1993 (first entry)

DE JAK2.

KW Phosphorylation; JAK1; JAK2; protein tyrosine kinase; human;

KW catalytic domain; SH2 domain; growth factor receptor; PTK; murine.

OS Mus musculus.

PH Key

FT Domain Location/Qualifiers

FT 402..663

FT /note= "Protein kinase domain 1"

FT Domain 706..979

FT /note= "Protein kinase domain 2"

PN W09210519-A.

PD 25-JUN-1992.

PF 26-NOV-1991; U08889.

PR 28-NOV-1990; AU-003594.

PA (LUDW-) LUDWIG INST CANCER RES.

PI Harpur A, Wilks AF, Ziemlecki A;

DR WPI; 92-234591/28.

DR N-PSDB; Q25307.

PT Novel protein tyrosine kinase mol. - comprises multiple catalytic

domains but no SH2 domain and is for phosphorylation of proteins

PS Claim 10; Fig 8; 50pp; English.

CC This sequence represents the murine protein tyrosine kinase JAK2 (from

CC Janus kinase). Northern analysis of JAK2 expression in a mouse

CC demonstrated the presence of two mRNA transcripts (4.8 and 4.4 kb).

CC The levels of these transcripts alter with respect to one another in

CC different tissues. The kidney, spleen and lung appear to express

CC predominantly the larger form, whereas ovary, placenta, skeletal muscle

CC and all murine cell lines analysed express both forms at equal levels.

CC The difference in sizes may be due to differential polyadenylation

CC sites. Both JAK2 and JAK1 are examples of a new subfamily or class

CC of protein tyrosine kinase. These can be used in the phosphorylation

CC of proteins, incorporation of labels and in the design of analogues,

CC antagonists and agonists of JAK's.

SQ Sequence 986 AA;

Query Match 36.2%; Score 51; DB 9; Length 986;

Best Local Similarity 55.8%; Pred. No. 7.71e+01;

Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Db 68 pkcvrakiv 76

| :|:|:|:|
 Qy 10 SKCVQKVE 18

RESULT 17

ID R15783 standard; Protein; 1100 AA.

AC R15783;

DT 10-FEB-1992 (first entry)

DE B.thuringiensis toxin/ACNPV gp64 fusion protein.

KW chimeric; fusion protein; insecticide; ACNPV; Lepidoptera larvae;

KW midgut targeting; bacterial endotoxin; pFav10.
 OS *Bacillus thuringiensis* var. *tenebriosis*.
 OS Autographa californica Nuclear Polyhedrosis Virus.
 PN W0911754-A.
 PD 14-NOV-1991.
 PF 02-MAY-1991; U03008.
 PR 03-MAY-1990; US-518575.
 PA (REGC) UNIV OF CALIFORNIA.
 PI Sivasubramanian N, Federici A;
 DR WPI: 91-353775/48.
 DR N-PSDB; Q14806.
 PT Extending host range or toxicity of insecticidal proteins - using
 PT protein capable of binding to gut epithelium of insects
 PS Claim 55; Fig 16; 61pp; English.
 CC A polylinker was inserted into the XmnI restriction site at the
 CC carboxyl terminus coding region of *B.thuringiensis* var. *tenebriosis*
 CC (Btt) toxin. DNA encoding the gp64 viral membrane protein of AcNPV
 CC was operably linked to the Btt toxin coding sequence via the
 CC polylinker. The gp64 gene sequences act as midgut targeting
 CC signals for bacterial endotoxins. Of three different Btt/gp64 gene
 CC fusions that were constructed, pFav10 was the longest. Its deduced
 CC amino acid sequence is given here.
 CC See also Q14807 and Q14808.
 SQ Sequence 1100 AA;

Query Match 36.2%; Score 51; DB 3; Length 1100;
 Best Local Similarity 45.5%; Pred. No. 7.71e+01;
 Matches 5; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Db 851 kfnrcirkvke 861
 | :|:|:|
 QY 8 KSSKCVQRKVE 18

RESULT 18
 ID R70830 standard; Protein; 1129 AA.

AC R70830;
 DT 06-OCT-1995 (first entry)
 DE Murine JAK2 kinase.
 KW JAK family; protein tyrosine kinase; cytokine receptor; mouse;
 KW phosphorylation; signal transduction; activation.
 OS *Mus musculus*.
 FH Key Location/Qualifiers
 FT Region 758..776
 FT /label= epitope
 FT Modified_site 1000-1015
 FT /label= autophosphorylation_site
 FT Misc difference 1..1129
 FT /note= "Amino acid sequence deduced from the
 FT published partial sequence of Jak2 cDNA
 FT (Harpur et al., Oncogene 7:1347-1353(1992))
 FT differs from R70830 in having the
 FT residues shown in brackets at the following
 FT positions: 154(S), 155(P), 337(T), 341(V),
 FT 473(S), 517(V), 522(L), 575(E), 731(F)."
 PN W09503701-A.
 PD 09-FEB-1995.
 PF 29-JUL-1994; U08676.
 PR 29-JUL-1993; US-097997.
 PA (SJUD-) ST JUDE CHILDREN'S RES HOSPITAL.
 PI Ihle JN, Quelle FW, Silvennoinen O, Witthuhn BA;
 DR WPI: 95-081950/11.
 DR N-PSDB; Q85412.
 PT Inhibiting a cellular response to a cytokine by inhibiting Jak
 PT kinase - to treat diseases caused by excessive response to
 PT cytokine, e.g. erythrocytosis and other cellular proliferative
 PT diseases

PS Claim 1; Fig 1; 167pp; English.
 CC Inhibiting the activity of a jak kinase (pref. Jak1, Jak2, Jak3 or
 CC Tyk2) in a eukaryotic cell is claimed as a method of inhibiting the
 CC biological response of that cell to a cytokine (not IL-3 or
 CC erythropoietin). The present sequence (murine JAK2 kinase) includes
 CC an epitopic sequence at amino acid positions 758-776. Antibodies which

CC selectively bind the epitope are able to bind Jak2 without interfering
 CC with the activity of the kinase. Such antibodies are claimed and are
 CC useful for detecting and extracting Jak2. There are 9 amino acid
 CC changes noted between the present sequence and the sequence deduced
 CC from the partial cDNA sequence published by Harpur et al., Oncogene 7:
 CC 1347-1353 (1992).
 SQ Sequence 1129 AA;

Query Match 36.2%; Score 51; DB 13; Length 1129;
 Best Local Similarity 55.6%; Pred. No. 7.71e+01;
 Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Db 211 pkcvrakiq 219
 :|:|:|:|
 QY 10 SKCVQRKVE 18

RESULT 19

ID R88123 standard; Protein; 1144 AA.
 AC R88123;
 DT 28-MAR-1996 (first entry)
 DE Tobacco mosaic virus resistance N gene protein.
 KW Tobacco mosaic virus resistance; TMV; N gene; Solanaceae;
 KW crop improvement; transgenic plant; crop improvement.
 OS Nicotiana glauca.
 FH Key Location/Qualifiers
 FT Region 1..150
 FT /label= Cytoplasmic_region
 FT Binding_site 216..224
 FT /label= P-loop
 FT /note= "ATP/GTP-binding site motif"
 FT Binding_site 228..229
 FT /label= P-loop
 FT /note= "ATP/GTP binding site motif"
 FT Binding_site 297..302
 FT /label= P-loop
 FT /note= "ATP/GTP binding site motif"
 FT Region 590..928
 FT /label= Leucine-rich_region
 FT /note= "the leucine-rich region (aa 590-928)
 FT includes 13 repeats of approx. 25 aa
 FT length"
 PN W09535024-A.
 PD 28-DEC-1995.
 PF 16-JUN-1995; U07754.
 PR 17-JUN-1994; US-261663.
 PA (REGC) UNIV CALIFORNIA.
 PA (USDA) US SEC OF AGRIC.
 PI Baker BJ, Whitham SA;
 DR WPI: 96-058144/06.
 DR N-PSDB; T09341.
 PT Plant virus resistance gene N sequences from tobacco - useful for
 PT generating transgenic Solanaceous plants resistant to Tobacco Mosaic
 PT Virus
 PS Claim 1; Page 65-70; 98pp; English.
 CC The Nicotiana glauca N gene protein (R88123) mediates
 CC resistance to tobacco mosaic virus (TMV). A cDNA clone (T09341)
 CC coding for the protein was obtd. from a N. glauca leaf cDNA
 CC library by transposon tagging. DNA sequences encoding the
 CC protein can be used to generate transgenic plants, esp. Solanaceae,
 CC resistant to TMV.
 SQ Sequence 1144 AA;

Query Match 36.2%; Score 51; DB 15; Length 1144;
 Best Local Similarity 25.0%; Pred. No. 7.71e+01;
 Matches 4; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

Db 156 dnrkdtdadcirqlid 171
 |:|:|:|:|
 QY 3 DHQGTSSKCVQRKVE 18

RESULT 20

FT	/note= "one of 21 complete segments of homology of 22 amino acid length"
FT	Region 736..757
FT	/label= tandem_repeat
FT	/note= "one of 21 complete segments of homology of 22 amino acid length"
FT	Region 758..779
FT	/label= tandem_repeat
FT	/note= "one of 21 complete segments of homology of 22 amino acid length"
FT	Region 780..801
FT	/label= tandem_repeat
FT	/note= "one of 21 complete segments of homology of 22 amino acid length"
FT	Region 802..823
FT	/label= tandem_repeat
FT	/note= "one of 21 complete segments of homology of 22 amino acid length"
FT	Region 824..845
FT	/label= tandem_repeat
FT	/note= "one of 21 complete segments of homology of 22 amino acid length"
FT	Region 846..867
FT	/label= tandem_repeat
FT	/note= "one of 21 complete segments of homology of 22 amino acid length"
FT	Region 868..889
FT	/label= tandem_repeat
FT	/note= "one of 21 complete segments of homology of 22 amino acid length"
FT	Region 890..911
FT	/label= tandem_repeat
FT	/note= "one of 21 complete segments of homology of 22 amino acid length"
FT	Region 912..933
FT	/label= tandem_repeat
FT	/note= "one of 21 complete segments of homology of 22 amino acid length"
FT	Region 934..946
FT	/label= partial_tandem_repeat
FT	Region 949..967
FT	/label= tandem_repeat
FT	/note= "one of 11 complete segments of homology of 19 amino acid length"
FT	Region 968..986
FT	/label= tandem_repeat
FT	/note= "one of 11 complete segments of homology of 19 amino acid length"
FT	Region 987..1005
FT	/label= tandem_repeat
FT	/note= "one of 11 complete segments of homology of 19 amino acid length"
FT	Region 1006..1024
FT	/label= tandem_repeat
FT	/note= "one of 11 complete segments of homology of 19 amino acid length"
FT	Region 1025..1043
FT	/label= tandem_repeat
FT	/note= "one of 11 complete segments of homology of 19 amino acid length"
FT	Region 1044..1062
FT	/label= tandem_repeat
FT	/note= "one of 11 complete segments of homology of 19 amino acid length"
FT	Region 1063..1081
FT	/label= tandem_repeat
FT	/note= "one of 11 complete segments of homology of 19 amino acid length"
FT	Region 1082..1100
FT	/label= tandem_repeat
FT	/note= "one of 11 complete segments of homology of 19 amino acid length"
FT	Region 1101..1119

FT	/label= tandem_repeat	
FT	/note= "one of 11 complete segments of homology	
FT	of 19 amino acid length"	
Region	1120..1138	
FT	/label= tandem_repeat	
FT	/note= "one of 11 complete segments of homology	
FT	of 19 amino acid length"	
Region	1139..1157	
FT	/label= tandem_repeat	
FT	/note= "one of 11 complete segments of homology	
FT	of 19 amino acid length"	
Region	1158..1173	
FT	/label= partial_tandem_repeat	
FT	/note= "partial segment of homology"	
Region	1179..1193	
FT	/label= tandem_repeat	
FT	/note= "one of 4 complete segments of homology	
FT	of 15 amino acid length"	
Region	1194..1208	
FT	/label= tandem_repeat	
FT	/note= "one of 4 complete segments of homology	
FT	of 15 amino acid length"	
Region	1209..1223	
FT	/label= tandem_repeat	
FT	/note= "one of 4 complete segments of homology	
FT	of 15 amino acid length"	
Region	1224..1238	
FT	/label= tandem_repeat	
FT	/note= "one of 4 complete segments of homology	
FT	of 15 amino acid length"	
Region	1248..1260	
FT	/label= tandem_repeat	
FT	/note= "one of 27 complete segments of homology	
FT	of 13 amino acid length"	
Region	1261..1273	
FT	/label= tandem_repeat	
FT	/note= "one of 27 complete segments of homology	
FT	of 13 amino acid length"	
Region	1274..1286	
FT	/label= tandem_repeat	
FT	/note= "one of 27 complete segments of homology	
FT	of 13 amino acid length"	
Region	1287..1299	
FT	/label= tandem_repeat	
FT	/note= "one of 27 complete segments of homology	
FT	of 13 amino acid length"	
Region	1300..1312	
FT	/label= tandem_repeat	
FT	/note= "one of 27 complete segments of homology	
FT	of 13 amino acid length"	
Region	1313..1325	
FT	/label= tandem_repeat	
FT	/note= "one of 27 complete segments of homology	
FT	of 13 amino acid length"	
Region	1326..1338	
FT	/label= tandem_repeat	
FT	/note= "one of 27 complete segments of homology	
FT	of 13 amino acid length"	
Region	1352..1364	
FT	/label= tandem_repeat	
FT	/note= "one of 27 complete segments of homology	
FT	of 13 amino acid length"	
Region	1365..1377	
FT	/label= tandem_repeat	
FT	/note= "one of 27 complete segments of homology	
FT	of 13 amino acid length"	
Region	1378..1390	
FT	/label= tandem_repeat	
FT	/note= "one of 27 complete segments of homology	

... Note: remainder of annotations omitted.

Query Match 36.28; Score 51; DB 9; Length 1663;
Best Local Similarity 31.6%; Pred. No. 7.71e+01;
Matches 6; Conservative 7; Mismatches 6; Indels 0; Gaps 0;

Db 44 esqdsseksikekvnea 62
QY 3 DHQGTSSKCVQRKVEGSS 21

RESULT 23

ID R50036 standard; Protein; 429 AA.
AC R50036;
DT 17-OCT-1994 (first entry)
DE Hantaan virus Nucleocapsid N protein.
KW Nucleocapsid N protein; G1; G2; glycoprotein; vector; vaccine;
OS diagnosis; Korean hemorrhagic fever; antibody.
OS Hantaan virus.

Key Location/Qualifiers

FT Misc_difference 122..123
FT /note= "Encoded by ACT ACT"
FT Misc_difference 195
FT /note= "Encoded by CTT"
FT Misc_difference 224
FT /note= "Encoded by GTT"
FT Misc_difference 233
FT /note= "Encoded by ATG"
FT Misc_difference 422
FT /note= "Encoded by TTC"
PN US5298423-A.
PD 29-MAR-1994.

PF 25-NOV-1987; 125105.
PR 25-NOV-1987; US-125105.
PR 14-NOV-1991; US-799479.
PA (USSA) US SEC OF ARMY.
PI Dairymple JM, Schmaljohn CS;
DR WPI: 94-100339/12.
DR N-PSDB; Q58735.
PT Vectors contg. coding sequences for the Hantaan virus
PT nucleocapsid N protein or G1 and G2 glyco-protein precursor -
PT generate viral proteins without having to propagate live
PT infectious virus
PS Disclosure; Fig 2; 23pp; English.
CC This sequence represents the Hantaan virus nucleocapsid N protein.
CC The cDNA encoding this sequence may be introduced into a vector for
CC the production of Hantaan virus proteins without the need to propagate
CC live virus. The expressed protein can be used in vaccines and
CC diagnostic applications for the study of Korean hemorrhagic fever.
CC The protein can also be injected into animals to raise antibodies
CC against the virus.
SQ Sequence 429 AA;

Query Match 34.8%; Score 49; DB 10; Length 429;
Best Local Similarity 35.0%; Pred. No. 1.24e+02;
Matches 7; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

Db 273 lgnmetkeskairghaeaa 292
QY 2 IDHQGTSSKCVQRKVEGSS 21

RESULT 24

ID R13794 standard; Protein; 487 AA.
AC R13794;
DT 29-NOV-1991 (first entry)
DE Drosophila hormone receptor 3.
KW Insect steroid receptor; DHR3.
OS Drosophila melanogaster.
FH Key Location/Qualifiers
FT Domain 51..116
FT /note= "zinc-finger DNA-binding domain C"

FT Domain 255..479
FT /note= "hormone-binding domain E"
PN W09113167-A.
PD 05-SEP-1991.
PF 15-FEB-1991; U01189.
PR 26-FEB-1990; US-485749.
PA (STRD) LELAND STANFORD JR UNIV.
PI Hogness DS, Koelle MR, Segraves WA;
DR WPI: 91-281480/38.
DR N-PSDB; Q13575.
PT DNA encoding insect steroid receptors - and ligands, for use as
PT benign inducing factors
PS Claim 24; Page 103; 126pp; English.
CC The amino acid sequence codes for Drosophila hormone receptor 3
CC protein which is part of the insect steroid receptor superfamily.
CC It can be used to screen for ligands specific for the insect
CC steroid receptors which can be used as highly specific and highly
CC active pesticides which are biodegradable. See also R13791-R13793.
SQ Sequence 487 AA;

Query Match 34.8%; Score 49; DB 3; Length 487;
Best Local Similarity 27.8%; Pred. No. 1.24e+02;
Matches 5; Conservative 7; Mismatches 6; Indels 0; Gaps 0;

Db 82 vynyqcpnrnkqcvdrvn 99
QY 1 VIDHQGTSSKCVQRKVE 18

RESULT 25

ID R04107 standard; protein; 694 AA.
AC R04107;
DT 13-SEP-1990 (first entry)
DE DNA-binding protein GCF represses transcription when bound to GC-rich seq
KW DNA-binding protein; GC-rich promoters; repression of transcription; ss
OS synthetic.

FH Key Location/Qualifiers

FT binding_site 359
FT /label= putative leucine zipper
FT binding_site 366
FT /label= putative leucine zipper
FT binding_site 373
FT /label= putative leucine zipper
FT binding_site 380
FT /label= putative leucine zipper
FT binding_site 719
FT /label= putative leucine zipper
FT binding_site 726
FT /label= putative leucine zipper
FT binding_site 733
FT /label= putative leucine zipper
FT binding_site 740
FT /label= putative leucine zipper
FT modified_site 394..396
FT /label= putative N-glycosylation site
FT modified_site 558..560
FT /label= putative N-glycosylation site
FT modified_site 637..639
FT /label= putative N-glycosylation site
FT modified_site 691..693
FT /label= putative N-glycosylation site
PN US7441912-A.

PD 06-MAR-1990.
PF 28-NOV-1989; 134593.
PR 28-NOV-1989; US-441912.
PA (USSH) US National Cancer Institute.
PI Pastan I, Kageyama R;
DR WPI: 90-132048/17.
DR N-NSDB; Q04026.
PT DNA binding protein recognises GC-rich sequences and represses
PT transcription from GC-rich promoters when bound to them
PS Disclosure; P; English.
CC The protein recognises GC-rich promoters including those of housekeeping

CC genes and cellular oncogenes.
SQ Sequence 694 AA;

Query Match 34.8%; Score 49; DB 1; Length 694;
Best Local Similarity 52.9%; Pred.No. 1.24e+02;
Matches 9; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Db 211 qdvkskstkstiqnless 227
QY 5 QGTSKSKCVQRKVEGSS 21

Search completed: Tue Jul 29 07:32:47 1997
Job time : 20 secs.

=> fil reg

FILE 'REGISTRY' ENTERED AT 10:20:16 ON 29 JUL 1997
 USE IS SUBJECT TO THE TERMS OF YOUR STN CUSTOMER AGREEMENT.
 PLEASE SEE "HELP USAGETERMS" FOR DETAILS.
 COPYRIGHT (C) 1997 American Chemical Society (ACS)

STRUCTURE FILE UPDATES: 27 JULY 97 HIGHEST RN 191786-00-2
 DICTIONARY FILE UPDATES: 28 JULY 97 HIGHEST RN 191786-00-2

TSCA INFORMATION NOW CURRENT THROUGH DECEMBER 1996

Please note that search-term pricing does apply when
 conducting SmartSELECT searches.

=> d que

L1 6 SEA FILE=REGISTRY ABB=ON VIDHQGTKSSKCVRQKVEGSS/SQSP

=> d sqide 1-6

L1 ANSWER 1 OF 6 REGISTRY COPYRIGHT 1997 ACS
 RN 173012-07-2 REGISTRY
 CN Complement C5, prepro- (human) (9CI) (CA INDEX NAME)
 FS PROTEIN SEQUENCE
 SQL 1676

```

SEQ      1 MGLLGILCFL IFLGKTWGQE QTYVISAPKI FRVGASENIV IQVYGYTEAF
      51 DATISIKSYP DKKFSYSSGH VHLSSSENKFQ NSAILTIQPK QLPGGQNPVS
     101 YVYLEVSKH FSKSKRMPIT YDNGFLFIHT DKPVYTPDQS VKVRVYSLND
     151 DLKPAKRETV LTFIDPEGSE VDMVEEIDHI GIISFPDFKI PSNPRYGMWT
     201 IKAKYKEDFS TTGTAYFEVK EYVLPHFSVS IEPEYNFIGY KNFKNFETIT
     251 KARYFYNKVV TEADVYITFG IREDLKDDQK EMMQTAMQNT MLINGIAQVT
     301 FDSETAVKEL SYYSLEDLNN KYLYIAVTVI ESTGGFSEEA EIPGIKYVLS
     351 PYKLNLVATP LFLKPGIPYP IKVQVKDSLQ QLVGGVPVIL NAQTIDVNQE
     401 TSDLDPSKSV TRVDDGVASF VLNLP SGVTV LEFNVKTDAP DLPEENQARE
     451 GYRAIAYSSL SQSYLYIDWT DNHKALLVGE HLNIIIVTPKS PYIDKITHYN
     501 YLILSKGKII HFGTREKFSD ASYQSINIPV TQNMVPSSRL LVYYIIVTGEQ
     551 TAEIVSDSVW LNIEEKCGNQ LQVHLSPDAD AYS PGQTVSL NMTATGMDSWV
     601 ALAAVDSAVY GVQRGAKKPL ERVFQFLEKS DLGCGAGGGL NNANVFHLAG
     651 LTFLTANANAD DSQENDEPCK EILRPRRTLQ KKIEEIAAKY KHSVVKKCCY
     701 DGACVNNDDET CEQRAARISL GPRCIKAFTE CCVVASQLRA NISHKDMQLG
     751 RLHMKTLTPV SKPEIRSYFP ESWLWEVHLV PRRKQLQFAL PDSLTTWEIQ
     801 GIGISNTGIC VADTVKAKVF KDVFLEMNIP YSVVRGEQIQ LKGTVYNYRT
     851 SGMQFCVKMS AVEGICTSES PVIDHQGTKS SKCVRQKVEG SSSHLVTFTV
           =====
     901 LPLEIGLHNI NFSLETWFGK EILVKTLRVV PEGVKRESYS GVTLDPRGIY
     951 GTISRRKEFP YRIPLDLVPK TEIKRILSVK GLLVGEILSA VLSQEGINIL
    1001 THLPKGSAEA ELMSVVPVIFY VFHYLETGNH WNIFHSDPLI EKQKLKKKLLK
    1051 EGMLSIMSYR NADYSYSVWK GGSASTWLTA FALRVLGQVN KYVEQNQNSI
    1101 CNSLLWLVEN YQLDNGSFKE NSQYQPIKLQ GTLPVEAREN SLYLTAFTVI
    1151 GIRKAFDICP LVKIDTALIK ADNFLLENTL PAQSTFTLAI SAYALSLGDK
    1201 THPQFRSIVS ALKREALVKG NPPIYRFWKD NLQHKDSSVP NTGTARMVET
    1251 TAYALLTSLN LKDINYVNPV IKWLSEEQRY GGGFYSTQDT INAIEGLTEY
    1301 SLLVKQLRLS MDIDVSYKHK GALHNYKMTD KNFLGRPVEV LLNDDLIVST
    1351 GFGSGLATVH VTTVVHKTST SEEVCSFYLK IDTQDIEASH YRGYGNSDYK
    1401 RIVACASYKP SREESSSGSS HAVMDISLPT GISANEEDLK ALVEGVDQLF
    1451 TDYQIKDGHV ILQLNSIPSS DFLCVRFRIF ELFEVGFSLP ATFTVYEHYR
    1501 PDKQCTMFYS TSNIKIQKVC EGAACKCVEA DCGQMQEELD LTISAETRKQ
    1551 TACKPEIAYA YKVSITSITV ENVFVKYKAT LLDIYKTGEA VAEKDSEITF
    1601 IKKVTCTNAE LVKGRQYLIM GKEALQIKYN FFSFRIIYPLD SLTWIEYWPR

```

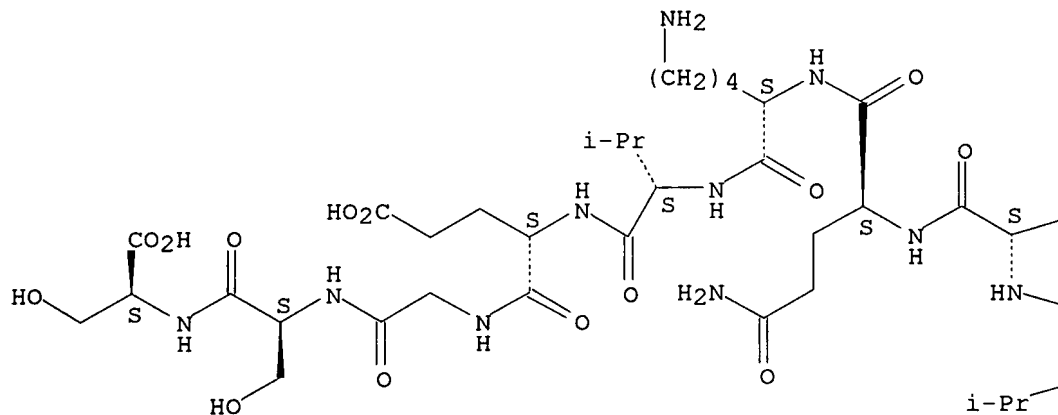
1651 DTTCSQCQAF LANLDEFAED IFLNGC
HITS AT: 872-892
MF Unspecified
CI MAN
SR CA
LC STN Files: CA, CAPLUS, TOXLIT
1 REFERENCES IN FILE CA (1967 TO DATE)
1 REFERENCES IN FILE CAPLUS (1967 TO DATE)

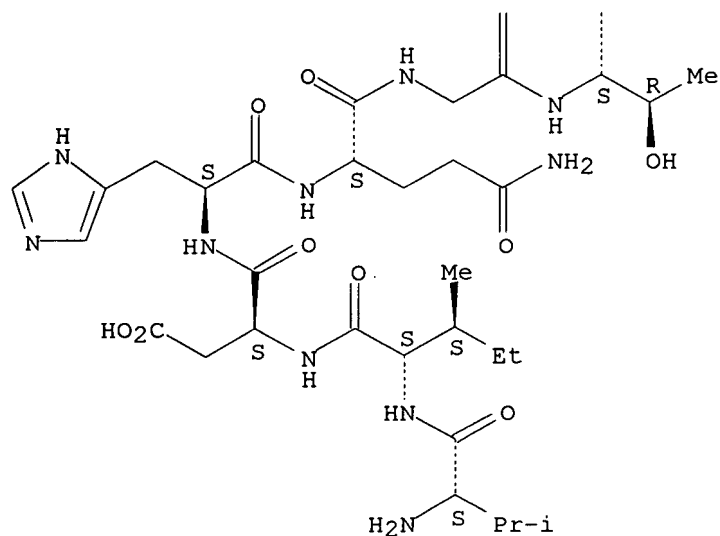
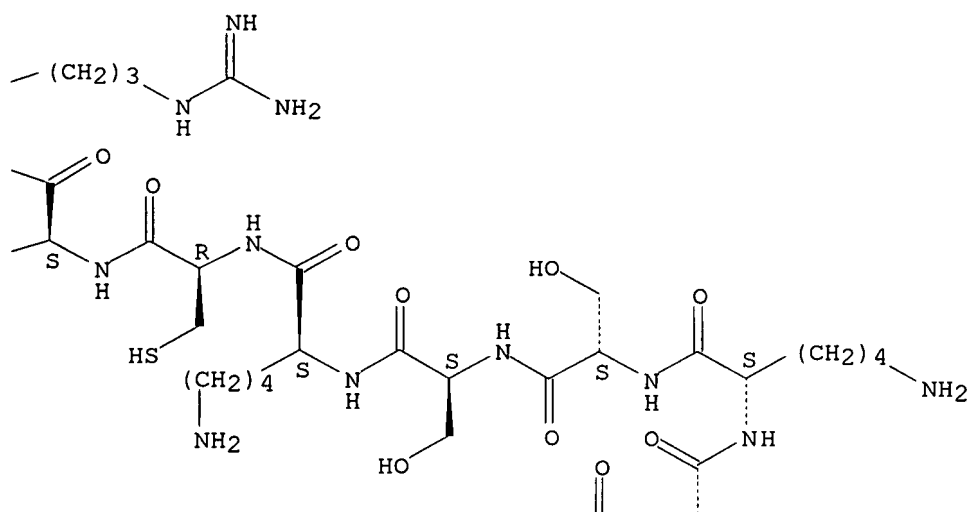
L1 ANSWER 2 OF 6 REGISTRY COPYRIGHT 1997 ACS
RN 172998-82-2 REGISTRY
CN L-Serine, L-valyl-L-isoleucyl-L-.alpha.-aspartyl-L-histidyl-L-glutaminyglycyl-L-threonyl-L-lysyl-L-seryl-L-seryl-L-lysyl-L-cysteinyl-L-valyl-L-arginyl-L-glutaminy-L-lysyl-L-valyl-L-.alpha.-glutamylglycyl-L-seryl- (9CI) (CA INDEX NAME)
FS PROTEIN SEQUENCE; STEREOSEARCH
SQL 21

SEQ 1 VIDHQGTKSS KCVRQKVEGS S
===== =
HITS AT: 1-21
MF C93 H161 N31 O33 S
SR CA
LC STN Files: CA, CAPLUS, TOXLIT

Absolute stereochemistry.

PAGE 1-A





1 REFERENCES IN FILE CA (1967 TO DATE)
1 REFERENCES IN FILE CAPLUS (1967 TO DATE)

L1 ANSWER 3 OF 6 REGISTRY COPYRIGHT 1997 ACS
RN 134774-08-6 REGISTRY
CN Complement C5, pro- (human clone pH5A/pC5HG2 protein moiety
reduced) (9CI) (CA INDEX NAME)

FS PROTEIN SEQUENCE
SQL 1658

```

SEQ      1 QEQTYVISAP KIFRVGASEN IVIQVYGYTE AFDATISIKS YPDKKFSYSS
      51 GHVHLSSEVK FQNSAILTIQ PKQLPGGQNP VSYVYLEVVS KHFSKSKRMP
     101 ITYDNGFLFI HTDKPVYTPD QSVKVRVYSL NDDLKPAKRE TVLTFIDPEG
     151 SEVDMVEEID HIGIISFPDF KIPSNPRYGM WTIKAKYKED FSTTGAYFE
     201 VKEYVLP HFS VSIEPEYNFI GYKNFKNF EI TIKARYFYNK VVTEADVYIT
     251 FGIREDLKDD QKEMMQTAMQ NTMLINGIAQ VTFDSETAVK ELSYYSLEDL
     301 NNKYLYIAVT VIESTGGFSE EAEIPGIKYV LSPYKLN LVA TPLFLKPGIP
     351 YPIKVQVKDS LDQLVGGVPV ILNAQTIDVN QETSDLDPSK SVTRVDDGVA
     401 SFVLNLPSGV TVLEFNVKTD APDLPEENQA REGYRAIAYS SLSQSYLYID
     451 WTDNHKALLV GEHLNIIIVT KSPYIDKITH YNYLILSKGK IIHFGTREKF
     501 SDASYQSINI PVTQNMVPSS RLLVYYIVTG EQTAEVSDS VWLNIEEKCG
     551 NQLQVHLSPD ADAYSPGQTV SLNMATGMDS WVALAAVDSA VYGVQRGAKK
     601 PLERVQFLE KSDLGCGAGG GLNNANVFHL AGLTFLTAN ADDSQENDEP
     651 CKEILRPRT LQKKIEEIAA KYKHSVVKKC CYDGACVNND ETCEQRAARI
     701 SLGPRCIKAF TECCVVASQL RANISHKDMQ LGR LHMKTLL PVSKPEIRSY
     751 FPESWLWEVH LVPRRKQLQF ALPDSLTTWE IQGIGISNTG ICVADTVKAK
     801 VFKDVFLEMN IPYSVVRGEQ IQLKGTVYNY RTSGMQFCVK MSAVEGICTS
     851 ESPVIDHQGT KSSKCVRQKV EGSSSHLVTF TVLPLEIGLH NINFSLETWF
          =====
     901 GKEILVKTLR VVPEGVKRES YSGVTLDPRG IYGTISRRKE FPYRIPLDLV
     951 PKTEIKRILS VKGLLVGFIL SAVLSQEGIN ILTHLPK GSA EAELMSVVPV
    1001 FYVFHYLETG NHWNIFHSDP LIEKQKLKKK LKEGMLSIMS VRNADYSYSV
    1051 WKGGSASTWL TAFALRVLGQ VNKYVEQNQN SICNSLLWL V ENYQLDNGSF
    1101 KENSQYQPIK LQGTLPVEAR ENSLYLTAFT VIGIRKAFDI CPLVKIDTAL
    1151 IKADNFLEN TLPAQSTFTL AISAYALSLG DKTHPQFRSI VSALKREALV
    1201 KGNPPIYRFW KDNLQHKDSS VPNTGTARMV ETTAYALLTS LNLKDINYVN
    1251 PVIKWLSEEQ RYGGGFYSTQ DTINAIEGLT EYSLLVKQLR LSMDIDVSYK
    1301 HKGALHNYKM TDKNFLGRPV EVLLNDDLIV STGFGSGLAT VHVTTVVHKT
    1351 STSEEVCSFY LKIDTQDIEA SHYRGYNSD YKRIVACASY KPSREESSSG
    1401 SSHAVMDISL PTGISANEED LKALVEGVDQ LFTDYQIKDG HVILQLNSIP
    1451 SSDFLCVRF R IFELFEVGFL SPATFTVY EY HRPDKQCTMF YSTSNIKI QK
    1501 VCEGAACKCV EADCGMQEE LDLTISAETR KQTACKPEIA YAYKVSITSI
    1551 TVENVFVKYK ATLLDIYKTG EAVAFKDSEI TFIKVTCTN AELVKGRQYL
    1601 IMGKEALQIK YNFSFRIYIP LDSLTWIEYW PRDTTCSSCQ AFLANLDEFA
    1651 EDIFLNGC

```

HITS AT: 854-874

MF Unspecified

CI MAN

SR CA

LC STN Files: CA, CAPLUS, TOXLIT

1 REFERENCES IN FILE CA (1967 TO DATE)

1 REFERENCES IN FILE CAPLUS (1967 TO DATE)

L1 ANSWER 4 OF 6 REGISTRY COPYRIGHT 1997 ACS

RN 134774-06-4 REGISTRY

CN Complement C5, prepro- (human clone pH5A/PC5HG2 protein moiety reduced) (9CI) (CA INDEX NAME)

FS PROTEIN SEQUENCE

SQL 1676

```

SEQ      1 MGLLGILCFL IFLGKTWGQE QTYVISAPKI FRVGASENIV IQVYGYTEAF
      51 DATISIKSY PDKKFSYSSGH VHLSEVKFQ NSAILTIQPK QLPGGQNPVS
     101 YVYLEVVS KH FSKSKRMPIT YDNGFLFIHT DKPVYTPDQS VKVRVYSLND
     151 DLKPAKRETV LTFIDPEGSE VDMVEEIDHI GIISFPDFKI PSNPRYGMWT
     201 IKAKYKEDFS TTGTAYFEVK EYVLP HFSVS IEPEYNFIGY KNFKNF EITI
     251 KARYFYNKVV TEADVYITFG IREDLKDDQK EMMQTAMQNT MLINGIAQVT

```

```

301 FDSETAVKEL SYYSLEDLNN KYLYIAVTVI ESTGGFSEEA EIPGIKYVLS
351 PYKLNLVATP LFLKPGIPYP IKVQVKDSLQ QLVGGVPVIL NAQTIDVNQE
401 TSDLDPSKSV TRVDDGVASF VLNLP SGVTV LEFNVKTDAP DLPEENQARE
451 GYRAIAYSSL SQSYLYIDWT DNHKALLVGE HLNIIIVTPKS PYIDKITHYN
501 YLILSKGKII HFGTREKFSD ASYQSINIPV TQNMVPSSRL LVYYIVTGEQ
551 TAEIVSDSVW LNIEEKCGNQ LQVHLSPAD AYSPGQTVSL NMATGMDSWV
601 ALAAVDSAVY GVQRGAKKPL ERVFQFLEKS DLGCGAGGGL NNANVFHLAG
651 LTFLTANAD DSQENDEPCK EILRPRRTLQ KKIEEIAAKY KHSVVKCCY
701 DGACVNNDET CEQRAARISL GPRCIKAFTE CCVVASQLRA NISHKDMQLG
751 RLHMKTLLPV SKPEIRSYFP ESWLWEVHLV PRRKQLQFAL PDSLTTWEIQ
801 GIGISNTGIC VADTVKAKVF KDVFLEMNIP YSVVRGEQIQ LKGTVYNYRT
851 SGMQFCVKMS AVEGICTSES PVIDHQGTKS SKCVRQKVEG SSSHLVTFTV
=====
901 LPLEIGHLNI NFSLETWFGK EILVKTLRVV PEGVKRESYS GVTLDPRGIY
951 GTISRRKEFP YRIPLDLVPK TEIKRILSVK GLLVGFIISA VLSQEGINIL
1001 THLPKGSAEA ELMSVVPVYF VFHYLETGNH WNIFHSDPLI EKQKLKKKLK
1051 EGMLSIMSVR NADYSYSVWK GGSASTWLTA FALRVLGQVN KYVEQNQNSI
1101 CNSLLWLVEN YQLDNGSFKE NSQYQPIKLQ GTLPVEAREN SLYLTAFTVI
1151 GIRKAFDICP LVKIDTALIK ADNFLLENTL PAQSTFTLAI SAYALSLGDK
1201 THPQFRSIVS ALKREALVKG NPPIYRFWKD NLQHKDSSVP NTGTARMVET
1251 TAYALLTSLN LKDINYVNPV IKWLSEEQRY GGGFYSTQDT INAIEGLTEY
1301 SLLVKQLRLS MDIDVSYKHK GALHNYKMTD KNFLGRPVEV LLNDDLIVST
1351 GFGSGLATVH VTTVVHKTST SEEVCSFYLK IDTQDIEASH YRGYGNNDYK
1401 RIVACASYKP SREESSSGSS HAVMDISLPT GISANEEDLK ALVEGVDQLF
1451 TDYQIKDGHV ILQLNSIPSS DFLCVRFRIF ELFEVGFSLP ATFTVYEHYR
1501 PDKQCTMFYS TSNIKIQKVC EGAACKCVEA DCGQMQEELD LTISAETRKQ
1551 TACKPEIAYA YKVSITSITV ENVFVKYKAT LLDIYKTGEA VAFKDSEITF
1601 IKKVTCTNAE LVKGRQYLIM GKEALQIKYN FSFRYIYPLD SLTWIEYWPR
1651 DTTCCSSCAF LANLDEFAD IFLNGC

```

HITS AT: 872-892

MF Unspecified

CI MAN

SR CA

LC STN Files: CA, CAPLUS, TOXLIT

1 REFERENCES IN FILE CA (1967 TO DATE)

1 REFERENCES IN FILE CAPLUS (1967 TO DATE)

L1 ANSWER 5 OF 6 REGISTRY COPYRIGHT 1997 ACS

RN 112548-72-8 REGISTRY

CN Complement C5b (human clone pC5HG2 .alpha.'-chain protein moiety reduced) (9CI) (CA INDEX NAME)

FS PROTEIN SEQUENCE

SQL 925

```

SEQ      1 LHMKTLLPVVS KPEIRSYFPE SWLWEVHLVP RRKQLQFALP DSLTTWEIQG
      51 IGISNTGICV ADTVKAKVFK DVFLEMNIPY SVVRGEQIQL KGTVYNYRTS
     101 GMQFCVKMSA VEGICTSESP VIDHQGTKSS KCVRQKVEGS SSSHLVTFTVL
=====
     151 PLEIGHLNIN FSLETWFGKE ILVKTLRVVP EGVKRESYSG VTLDPRGIYG
     201 TISRRKEFPY RIPLDLVPKT EIKRILSVKG LLVGEILSAV LSQEGINILT
     251 HLPKGSAAEA LMSVVPVYFV FHYLETGNHW NIFHSDPLIE KQKLKKKLKE
     301 GMLSIMSYRN ADYSYSVWK GASTWLTAF ALRVLGQVNK YVEQNQNSIC
     351 NSLLWLVEN YQLDNGSFKEN SQYQPIKLQ TLPVEARENS LYLTAFTVIG
     401 IRKAFDICPL VKIDTALIK ADNFLLENTL PAQSTFTLAIS AYALSLGDKT
     451 HPQFRSIVSA LKREALVKG NPIYRFWKD NLQHKDSSVPN TGTARMVETT
     501 AYALLTSLNL KDINYVNPVI KWLSEEQRYG GGFYSTQDTI NAIEGLTEYS
     551 LLVKQLRLSM DIDVSYKHK GALHNYKMTD NFLGRPVEVL LNDDLIVSTG
     601 FGSGLATVHV TTVVHKTSTS EEVCSFYLKI DTQDIEASHY RGYGNNDYKR
     651 IVACASYKPS REESSSGSSH AVMDISLPTG ISANEEDLKA LVEGVDQLFT

```

Gambel 08/487,283

701 DYQIKDGHVI LQLNSIPSSD FLCVRFRIFE LFEVGFSLSPA TFTVYEHYHRP
751 DKQCTMFYST SNIKIQKVCE GAACKCVEAD CGDMQEELDL TISAETRKQT
801 ACKPEIAYAY KVSITSITVE NVFVKYKATL LDIYKTGEAV AEKDSEITFI
851 KKVTTCTNAEL VKGRQYLIMG KEALQIKYNF SFRYIYPLDS LTWIEYWPRD
901 TTCSSCQAFI ANLDEFAEDI FLNGC

HITS AT: 121-141

MF Unspecified

CI MAN

SR CA

LC STN Files: CA, CAPLUS, CJACS, TOXLIT

1 REFERENCES IN FILE CA (1967 TO DATE)

1 REFERENCES IN FILE CAPLUS (1967 TO DATE)

L1 ANSWER 6 OF 6 REGISTRY COPYRIGHT 1997 ACS

RN 112548-71-7 REGISTRY

CN Complement C5 (human clone pC5HG2 .alpha.-chain protein moiety
reduced) (9CI) (CA INDEX NAME)

FS PROTEIN SEQUENCE

SQL 999

SEQ 1 TLQKKIEEIA AKYKHSVVKK CCYDGACVNN DETCEQRAAR ISLGPRCIKA
51 FTECCVVASQ LRANISHKDM QLGRHLMKTL LPVSKPEIRS YFPESWLWEV
101 HLVPRRKQLQ FALPDSLTTW EIQQIGISNT GICVADTVKA KVFKDVFLEM
151 NIPYSVVRGE QIQLKGTVYN YRTSGMQFCV KMSAVEGICT SESPVIDHQG

=====

201 TKSSKCVRQK VEGSSSHLVT FTVLPLEIGL HNINFSLETW FGKEILVKTL
=====

251 RVVPEGVKRE SYSGVTLDPR GIYGTISRRK EFPYRIPLDL VPKTEIKRIL
301 SVKGLLVGEI LSAVLSQEGI NILTHLPKGS AEAELMSVVP VFYVFHYLET
351 GNHWNIFHSD PLIEKQKLKK KLKEGMLSIM SYRNADYSYS VWKGGSASTW
401 LTAFALRVLG QVNKYVEQNQ NSICNSLLWL VENYQLDNGS FKENSQYQPI
451 KLQGTLPVEA RENSPLYTAF TVIGIRKAFD ICPLVKIDTA LIKADNFLLE
501 NTLPAQSTFT LAISAYALSL GDKTHPQFRS IVSALKREAL VKGNPPIYRF
551 WKDNLQHKDS SVPNTGTARM VETTAYALLT SLNLKDINYV NPVIKWLSEE
601 QRYGGGFYST QDTINAIEGL TEYSLLVKQL RLSMDIDVSY KHKGALHNYK
651 MTDKNFLGRP VEVLLNDDLI VSTGFGSGLA TVHVTTVVHK TSTSEEVCSF
701 YLKIDTQDIE ASHYRGYGNs DYKRIVACAS YKPSREESSG GGGHAVMDIS
751 LPTGISANEE DLKALVEGVD QLFTDYQIKD GHVILQLNSI PSSDFLCVRF
801 RIFELFEVGF LSPATFTVYE YHRPDQCTM FYSTSNIKIQ KVCEGAACKC
851 VEADCGQMQE ELDLTISAET RKQTACKPEI AYAYKVSITG ITVENVFVKY
901 KATLLDIYKT GEAVAEDSE ITFIKVTCT NAELVKGRQY LIMGKEALQI
951 KYNFSFRYIY PLDSLWIEY WPRDTTCSSC QAFLANLDEF AEDIFLNGC

HITS AT: 195-215

MF Unspecified

CI MAN

SR CA

LC STN Files: CA, CAPLUS, CJACS, TOXLIT

2 REFERENCES IN FILE CA (1967 TO DATE)

2 REFERENCES IN FILE CAPLUS (1967 TO DATE)

=> fil hcaplus

FILE 'HCAPLUS' ENTERED AT 10:20:41 ON 29 JUL 1997

USE IS SUBJECT TO THE TERMS OF YOUR STN CUSTOMER AGREEMENT.

PLEASE SEE "HELP USAGETERMS" FOR DETAILS.

COPYRIGHT (C) 1997 AMERICAN CHEMICAL SOCIETY (ACS)

Copyright of the articles to which records in this database refer is held by the publishers listed in the PUBLISHER (PB) field (available for records published or updated in Chemical Abstracts after December

26, 1996), unless otherwise indicated in the original publications.

FILE COVERS 1967 - 29 Jul 1997 VOL 127 ISS 5
FILE LAST UPDATED: 29 Jul 1997 (970729/ED)

This file contains CAS Registry Numbers for easy and accurate
substance identification.
'OBI' IS DEFAULT SEARCH FIELD FOR 'HCAPLUS' FILE

=> s ll

L2 3 L1

=> d .ca 1-3

L2 ANSWER 1 OF 3 HCAPLUS COPYRIGHT 1997 ACS

AN 1996:73261 HCAPLUS

DN 124:127101

TI Anti-complement C5 antibodies for the treatment of
glomerulonephritis and other inflammatory diseases

IN Evans, Mark J.; Matis, Louis; Mueller, Eileen Elliott; Nye, Steven
H.; Rollins, Scott; Rother, Russell P.; Springhorn, Jeremy P.;
Squinto, Stephen P.; Thomas, Thomas C.; et al.

PA Alexion Pharmaceuticals, Inc., USA

SO PCT Int. Appl., 159 pp.

CODEN: PIXXD2

PI WO 9529697 A1 951109

DS W: AM, AU, BB, BG, BR, BY, CA, CN, CZ, EE, FI, GE, HU, IS, JP, KG,
KP, KR, KZ, LK, LR, LT, LV, MD, MG, MN, MX, NO, NZ, PL, RO, RU,
SG, SI, SK, TJ, TM, TT, UA, UG, US, UZ, VN

RW: AT, BE, BF, BJ, CF, CG, CH, CI, CM, DE, DK, ES, FR, GA, GB, GR,
IE, IT, LU, MC, ML, MR, NE, NL, PT, SE, SN, TD, TG

AI WO 95-US5688 950501

PRAI US 94-236208 940502

DT Patent

LA English

AB The use of anti-C5 antibodies, e.g., monoclonal antibodies, to treat
glomerulonephritis (GN) is disclosed. The administration of such
antibodies at low dosage levels has been found to significantly
reduce glomerular inflammation/enlargement and other pathol.
conditions assocd. with GN. Also disclosed are novel anti-C5
antibodies and anti-C5 antibody-encoding nucleic acid mols. These
antibodies are useful in the treatment of GN and other inflammatory
conditions involving pathol. activation of the complement system.

IT **173012-07-2**, Complement C5, prepro- (human)

RL: BOC (Biological occurrence); PRP (Properties); THU (Therapeutic
use); BIOL (Biological study); OCCU (Occurrence); USES (Uses)
(amino acid sequence; anti-complement C5 antibodies for the
treatment of glomerulonephritis and other inflammatory diseases)

IT **172998-82-2P**

RL: BPN (Biosynthetic preparation); PRP (Properties); THU
(Therapeutic use); BIOL (Biological study); PREP (Preparation); USES
(Uses)
(epitope KSSKC-contg. antigen; anti-complement C5 antibodies for
the treatment of glomerulonephritis and other inflammatory
diseases)

IC ICM A61K038-36

ICS A61K039-00; A61K039-395; C07K014-00; C07K014-75; C07K016-00;
C07K016-18; C07K016-36; C07K016-46; C12N005-10; C12N005-20;
C12N015-09; C12N015-10; C12N015-13; C12N015-63; C12P021-02;

C12P021-08

CC 63-3 (Pharmaceuticals)
Section cross-reference(s): 3, 15

IT **173012-07-2**, Complement C5, prepro- (human)
RL: BOC (Biological occurrence); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); OCCU (Occurrence); USES (Uses)
(amino acid sequence; anti-complement C5 antibodies for the treatment of glomerulonephritis and other inflammatory diseases)

IT **172998-82-2P**
RL: BPN (Biosynthetic preparation); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); USES (Uses)
(epitope KSSKC-contg. antigen; anti-complement C5 antibodies for the treatment of glomerulonephritis and other inflammatory diseases)

L2 ANSWER 2 OF 3 HCAPLUS COPYRIGHT 1997 ACS
AN 1991:442982 HCAPLUS
DN 115:42982
TI Complete cDNA sequence of human complement pro-C5. Evidence of truncated transcripts derived from a single copy gene
AU Haviland, David L.; Haviland, Joie C.; Fleischer, Daniel T.; Hunt, Allison; Wetsel, Rick A.
CS Sch. Med., Washington Univ., St. Louis, MO, 63110, USA
SO J. Immunol. (1991), 146(1), 362-8
CODEN: JOIMA3; ISSN: 0022-1767
DT Journal
LA English
AB Two truncated human C5 clones, pHC5A and pHC5B, were isolated from an adult human liver cDNA library, and contained inserts of 2930 and 2181 bp, resp. Both clones were polyadenylated and encoded the 5'-end of the C5 pro-mol., thereby completing the human pro-C5 cDNA sequence. However, near the 3'-ends, at exon/intron boundaries, the nucleotide sequences of pHC5A and pHC5B diverged from each other and from the full-length 6.0-kb C5 cDNA sequence. Clone pHC5A, which overlapped the first human C5 clone described (J-16), encoded most of the C5 signal peptide, the complete .beta.-chain, the linker peptide, 177 amino acids of the .alpha.-chain, and contained 144 bp of Alu family consensus sequence encoding 48 amino acids of divergent protein sequence in an open reading frame. Clone pHC5B encoded the entire C5 signal peptide, the .beta.-chain, the linker peptide, 9 amino acids of the .alpha.-chain, and 6 amino acids of divergent protein sequence in an open reading frame. Northern blot expts. demonstrated the presence of a 3.0-kb truncated C5 mRNA in adult human liver and a 4.8-kb truncated C5 mRNA in HepG2 cells in addn. to the 6.0-kb full-length transcript. Truncated C5 mRNA were not detected in Raji, MOLT-4, human fibroblast or U937 cells, although the full-length 6.0-kb transcript was seen in MOLT-4 cells. Southern blot analyses indicated that the human C5 structural gene is large, complex, and is present in the human genome in a single copy, thereby demonstrating that the truncated C5 clones and mRNA are derived from a single C5 gene by alternative processing events.

IT **112548-71-7**, Complement C 5 (human clone pC5HG2 .alpha.-chain protein moiety reduced) **134774-06-4**
134774-08-6
RL: PRP (Properties)
(amino acid sequence of)

CC 3-3 (Biochemical Genetics)
Section cross-reference(s): 13, 15

IT **112548-71-7**, Complement C 5 (human clone pC5HG2 .alpha.-chain protein moiety reduced) 134774-03-1, Complement C 5 (human clone pHC5A/pC5HG2 .beta.-chain protein moiety reduced) 134774-04-2, Complement C 5 (human clone pHC5B protein moiety reduced) 134774-05-3 **134774-06-4** 134774-07-5 **134774-08-6** 134774-09-7 134774-10-0
 RL: PRP (Properties)
 (amino acid sequence of)

L2 ANSWER 3 OF 3 HCAPLUS COPYRIGHT 1997 ACS
 AN 1988:107290 HCAPLUS
 DN 108:107290
 TI Molecular analysis of human complement component C5: localization of the structural gene to chromosome 9
 AU Wetsel, Rick A.; Lemons, Richard S.; Le Beau, Michelle M.; Barnum, Scott R.; Noack, Deborah; Tack, Brian F.
 CS Dep. Immunol., Res. Inst. Scripps Clin., La Jolla, CA, 92037, USA
 SO Biochemistry (1988), 27(5), 1474-82
 CODEN: BICHAW; ISSN: 0006-2960
 DT Journal
 LA English
 OS CJACS
 AB A human C5 clone (pC5HG2) was isolated from a cDNA library constructed from HepG2 mRNA. The DNA sequence showed that the pC5HG2 insert was comprised of 3309 base pairs of pro-C5 coding sequence and 404 base pairs of 3'-untranslated sequence. The derived amino acid sequence contained the entire coding sequence of the C5 .alpha.-chain, the .beta.-.alpha.-chain junction region, and 100 amino acids (.apprx.50%) of the .beta.-chain. Protein sequences of 4 C5 tryptic peptides were aligned exactly to this sequence and demonstrated that C5 synthesized and secreted by HepG2 cells is probably identical with plasma-derived C5. Coding sequence alignment of the human C5 sequences with those of murine C5 indicated that 80% of the nucleotides and 79% of the amino acids were placed identically in the 2 species. Amino acid sequence alignment of the homologous family members C3, C4, and .alpha.2-macroglobulin with that of C5 demonstrated 27%, 25%, and 19% identity, resp. As was found in murine C5, the corresponding thiol ester region of human C5 contained several conserved amino acids, but the crit. cysteine and glutamine residues which give rise to the intramol. thiol ester bond in C3, C4, and .alpha.2-macroglobulin were absent in C5, having been replaced by serine and alanine, resp. With the use of a panel of hamster-human somatic cell hybrids, the C5 gene was mapped to human chromosome 9. In situ chromosomal hybridization studies employing metaphase cells further localized the gene to bands 9q32-34, with the largest cluster of grains at 9q34.1.

IT **112548-71-7 112548-72-8**
 RL: PRP (Properties)
 (amino acid sequence of)

CC 3-3 (Biochemical Genetics)
 Section cross-reference(s): 13, 15

IT **112548-71-7 112548-72-8**
 RL: PRP (Properties)
 (amino acid sequence of)

Gambel 08/487,283

=> fil wpids

FILE 'WPIDS' ENTERED AT 09:54:32 ON 29 JUL 1997
COPYRIGHT (C) 1997 DERWENT INFORMATION LTD

FILE LAST UPDATED: 23 JUL 97 <970723/UP>
>>>UPDATE WEEKS:
MOST RECENT DERWENT WEEK 9730 <199730/DW>
DERWENT WEEK FOR CHEMICAL CODING: 9724
DERWENT WEEK FOR POLYMER INDEXING: 9727
DERWENT WORLD PATENTS INDEX SUBSCRIBER FILE, COVERS 1963 TO DATE
>>> D COST AND SET NOTICE DO NOT REFLECT SUBSCRIBER DISCOUNTS -
SEE HELP COST FOR DETAILS <<<
>>> PCT PUBLICATIONS FROM 19 DECEMBER 1996 - SEE NEWS <<<

=> d que l6;d his l7-

L1 66 SEA FILE=WPIDS ABB=ON "EVANS M"/AU OR ("EVANS M J"/AU OR
"EVANS M J W"/AU)
L2 5 SEA FILE=WPIDS ABB=ON ("MATIS L"/AU OR "MATIS L A"/AU)
L3 303 SEA FILE=WPIDS ABB=ON "MUELLER E"/AU OR "MUELLER E E"/AU

L4 5 SEA FILE=WPIDS ABB=ON "NYE S"/AU OR "NYE S H"/AU
L5 12 SEA FILE=WPIDS ABB=ON ("ROLLINS S"/AU OR "ROLLINS S A"/A
U OR "ROLLINS S M"/AU OR "ROLLINS S S"/AU)
L6 381 SEA FILE=WPIDS ABB=ON L1 OR L2 OR L3 OR L4 OR L5

(FILE 'WPIDS' ENTERED AT 09:49:50 ON 29 JUL 1997)

L7 24 S COMPLEMENT AND C5
L8 3 S L7 AND L6
L9 309 S ALPHA (2W) CHAIN#
L10 1 S L7 AND L9
L11 14151 S HIS
L12 4 S L7 AND (NTIBOD? OR ANTI)
L13 8 S L7 AND (ANTIBOD? OR ANTI)
L14 8 S L13 OR L10
L15 0 S L8 NOT L14

FILE 'WPIDS' ENTERED AT 09:52:49 ON 29 JUL 1997

FILE 'WPIDS' ENTERED AT 09:54:32 ON 29 JUL 1997

=> d .wp 1-8 l14

L14 ANSWER 1 OF 8 WPIDS COPYRIGHT 1997 DERWENT INFORMATION LTD
AN 96-188197 [19] WPIDS
DNC C96-060068
TI Treatment of inflammatory joint disease with C5 blocker -
which inhibits cell lysing ability of complement complex
in e.g. rheumatoid arthritis or osteoarthritis.
DC B05
IN MATIS, L; WANG, Y
PA (ALEX-N) ALEXION PHARM INC
CYC 19
PI WO 9609043 A1 960328 (9619)* EN 70 pp
RW: AT BE CH DE DK ES FR GB GR IE IT LU MC NL PT SE
W: AU CA JP
AU 9537292 A 960409 (9629)
EP 777474 A1 970611 (9728) EN

R: DE ES FR GB NL

ADT WO 9609043 A1 WO 95-US12404 950921; AU 9537292 A AU 95-37292 950921;
EP 777474 A1 EP 95-935171 950921, WO 95-US12404 950921
FDT AU 9537292 A Based on WO 9609043; EP 777474 A1 Based on WO 9609043
PRAI US 94-311489 940923
AB WO 9609043 A UPAB: 960510

Treating established joint inflammation in a human or non-human patient comprises administering an **anti**-inflammatory amt. of a **C5** blocker. Also claimed is a pharmaceutical agent contained within packaging material where: (a) the pharmaceutical agent comprises a **C5** blocker which provides the agent with **anti**-inflammatory properties and (b) the packaging material comprises a label which indicates that the pharmaceutical agent is for use in the treatment of joint inflammation and/or of arthritis.

USE - The types of joint inflammation diseases which may be treated are rheumatoid arthritis and juvenile onset rheumatoid arthritis and also osteoarthritis.

ADVANTAGE - Admin. of the **C5** blockers arrests and/or reduces inflammation in joints which are already inflamed and inhibits the spread of inflammation to unaffected joints.
Dwg.5A/10

L14 ANSWER 2 OF 8 WPIDS COPYRIGHT 1997 DERWENT INFORMATION LTD

AN 95-392923 [50] WPIDS

DNC C95-169278

TI Treating glomerulonephritis with **antibody** against **complement C5** component - to inhibit **complement** induced cell lysis.

DC B04 D16

IN EVANS, M J; MATIS, L; MUELLER, E E; NYE, S H; ROLLINS, S; ROTHER, R P; SPRINGHORN, J P; SQUINTO, S P; THOMAS, T C; WANG, Y; WILKINS, J A

PA (ALEX-N) ALEXION PHARM INC

CYC 15

PI WO 9529697 A1 951109 (9550)* EN 181 pp
AU 9524747 A 951129 (9609)
EP 758904 A1 970226 (9714) EN

R: AT BE CH DE DK ES FR GB IE IT LI NL PT SE

ADT WO 9529697 A1 WO 95-US5688 950501; AU 9524747 A AU 95-24747 950501;
EP 758904 A1 EP 95-919041 950501, WO 95-US5688 950501

FDT AU 9524747 A Based on WO 9529697; EP 758904 A1 Based on WO 9529697

PRAI US 94-236208 940502

AB WO 9529697 A UPAB: 951215

Glomerulonephritis (GN) is treated by admin. of an **antibody** (Ab) that binds to **complement** component **C5** in the blood to reduce the cell-lysing activity of **complement**. Also new are: (1) Ab specific for the **alpha chain** of human **C5**, able to inhibit **complement** activated lysis but unable to bind specifically to the free C5a activation product; (3) the hybridoma 5G1.1 (ATCC HB.11625); (4) Abs produced by this hybridoma or **antibodies** able to compete with it for binding to **C5 alpha chain**; (5) a nucleic acid (I) encoding a single chain (sc) Fv polypeptide of 248 amino acids.

USE - The Abs practically eliminate glomerular inflammation and enlargement associated with GN, and can also be used wherever inhibition of **complement** is required, e.g. in cases of inflammatory joint disease or in treatment of immunological or haematological disorders associated with extracorporeal circulation. The isolated **alpha chain** of **C5** and

peptides can be used to induce prodn. of Ab by immunisation, or to screen candidate **antibodies** for **anti-C5** activity.

ADVANTAGE - Ab are specific for **C5** and do not affect opsonic, **anti-infective** and immune complex clearance functions of **complement**. Some Abs block haemolysis by **complement** at close to the theoretical 1:2 **antibody**:antigen ratio.
Dwg.0/19

L14 ANSWER 3 OF 8 WPIDS COPYRIGHT 1997 DERWENT INFORMATION LTD

AN 95-351129 [45] WPIDS

DNC C95-153772

TI Redn. of immune/haemostatic dysfunction during extracorporeal circulation - by admin. of an **anti-C5 antibody** to reduce e.g. **complement**, platelet or leukocyte activation and/or platelet-leukocyte adhesion.

DC B04

IN ROLLINS, S A; SMITH, B R; SQUINTO, S P

PA (ALEX-N) ALEXION PHARM INC; (UYYA) UNIV YALE

CYC 6

PI WO 9525540 A1 950928 (9545)* EN 35 pp

AU 9521917 A 951009 (9603)

EP 751787 A1 970108 (9707) EN

R: DE ES FR GB NL

ADT WO 9525540 A1 WO 95-US3614 950322; AU 9521917 A AU 95-21917 950322;

EP 751787 A1 EP 95-914820 950322, WO 95-US3614 950322

FDT AU 9521917 A Based on WO 9525540; EP 751787 A1 Based on WO 9525540

PRAI US 94-217391 940323

AB WO 9525540 A UPAB: 951114

The following are claimed: (A) a method for performing a therapeutic procedure on a patient, which comprises: (a) passing circulating blood from a blood vessel of the patient through a conduit (which has a luminal surface comprising a material capable of causing **complement** activation (CA), platelet activation (PA), leukocyte activation (LA) and/or platelet-leukocyte adhesion (PLA) in the patient's blood) and back to a blood vessel of the patient, and (b) introducing an **antibody** which specifically binds to **complement** component **C5**, into the patient's bloodstream, in an amt. effective to reduce CA, PA, LA and/or PLA resulting from passage of the circulating blood through the conduit; step (a) occurs before, during and/or after step (b); (B) an article of manufacture comprising packaging material and a pharmaceutical agent contained within the packaging material, where: (a) the pharmaceutical agent comprises an **antibody** as above, and (b) the packaging material comprises a label which indicates that the pharmaceutical agent is for use with an extracorporeal circulation procedure.

USE - The method can be used to perform a cardiopulmonary bypass procedure (claimed). More generally, the process may be used to reduce dysfunction of the immune and haemostatic systems, associated with extracorporeal circulation (ECC). These include e.g. the development of inflammation, platelet dysfunction and thrombocytopenia.

ADVANTAGE - No further details.
Dwg.0/4

L14 ANSWER 4 OF 8 WPIDS COPYRIGHT 1997 DERWENT INFORMATION LTD

AN 95-139556 [18] WPIDS

DNC C95-064463
 TI Chimeric proteins which inhibit **complement** activation -
 useful for the treatment of **complement** mediated
 inflammation and auto immune diseases..
 DC B04 D16
 IN HIGGINS, P J; KO, J; YEH, C G
 PA (CYTO-N) CYTOMED INC
 CYC 21
 PI WO 9508570 A1 950330 (9518)* EN 74 pp
 RW: AT BE CH DE DK ES FR GB GR IE IT LU MC NL PT SE
 W: AU CA CN JP
 AU 9480719 A 950410 (9530)
 EP 723555 A1 960731 (9635) EN
 R: AT BE CH DE DK ES FR GB GR IE IT LI LU MC NL PT SE
 JP 09502985 W 970325 (9722) 62 pp
 ADT WO 9508570 A1 WO 94-US10786 940923; AU 9480719 A AU 94-80719 940923;
 EP 723555 A1 EP 94-931763 940923, WO 94-US10786 940923; JP 09502985
 W WO 94-US10786 940923, JP 95-509957 940923
 FDT AU 9480719 A Based on WO 9508570; EP 723555 A1 Based on WO 9508570;
 JP 09502985 W Based on WO 9508570
 PRAI US 93-126596 930924; US 94-310416 940922
 AB WO 9508570 A UPAB: 950518

A chimeric protein (CP) is claimed which comprises a first
 polypeptide (PP1) which inhibits **complement** activation,
 linked to a second polypeptide (PP2) which inhibits
complement activation, where PP1 and PP2 can be the same or
 different. Also claimed are: (1) a nucleic acid encoding a CP where
 PP1 and PP2 are linked by a peptide bond; (2) a recombinant
 expression vector comprising a selectable marker and the nucleic
 acid of (1) operably linked to regulatory sequences for the
 expression of the CP; (3) a process for preparing a recombinant CP
 comprising culturing a suitable host cell comprising the vector of
 (2) under conditions promoting expression; (4) a method of
 inhibiting C3a and C5a generation comprising: (a) contacting a C3
 convertase with the CP; (b) contacting a C5 convertase
 with the CP, where binding of the CP with the C3 convertase and
 C5 convertase inhibits the generation of C3a and C5a
 respectively; and (5) an **antibody** which binds to the
 soluble CP but does not bind to PP1 or PP2 alone.

USE - The CPs may be used for reducing inflammation
 characterised by excessive **complement** activation
 (claimed). The CPs may also be used in the treatment of autoimmune
 diseases. Monoclonal **antibodies** directed against the CPs
 may be used as diagnostic or therapeutic agents. The CPs can be
 combined with an appropriate pharmaceutical formulation and
 administered by a variety of routes including intravenous bolus
 injection, intravenous infusion, intraperitoneal, intradermal,
 intramuscular, subcutaneous, intranasal and oral routes.
 Dwg.0/15

L14 ANSWER 5 OF 8 WPIDS COPYRIGHT 1997 DERWENT INFORMATION LTD
 AN 91-038259 [06] WPIDS
 DNN N91-029558 DNC C91-016357
 TI Sensitive assay of C5a **complement** peptide - by reaction
 with immobilised specific **antibody**, detectable
antibody, and monoclonal **antibodies**, for treating
 sepsis, etc..
 DC B04 D16 J04 S03
 IN GOTZE, O; OPPERMANN, M; SCHULZE, M

PA (GOTZ-I) GOTZE O

CYC 9

PI EP 411306 A 910206 (9106)*

R: BE CH DE FR GB IT LI NL SE

DE 3924924 A 910207 (9107)

ADT EP 411306 A EP 90-111920 900622; DE 3924924 A DE 89-3924924 890727

PRAI DE 89-3924924 890727

AB EP 411306 A UPAB: 930928

Detection and/or quantitative determination of the **complement** peptides C5a and/or C5a-des-Arg (C5a') in biological fluid comprises: (1) contacting test sample with a matrix to which **antibodies** (Ab1), able to bind C5a and/or C5a' are fixed; (2) contacting the incubated matrix with second detectable **antibodies** (Ab2), or their fragments, which bind to native C5, C5a and/or C5a' and (3) detecting Ab2 or its fragments. Also new are (1) test kits for this process; (2) cell lines producing monoclonal **antibodies** (MAb) which bind, in C5a and C5a' to the receptor binding site for the C5a-specific receptors, but not with the corresponding amino acid sequence in native C5; (3) MAb produced by these cell lines, (4) **anti-idiotypic antibodies** (AIAb) against MAb produced by the specified cell lines, and (5) the cell line CNCM I-188 which produces the AIAb F23/14.

USE/ADVANTAGE - This method provides reliable and sensitive assay of C5a and C5a' with detection sensitivity 20 pg/ml (compare 1 ng/ml for the known process), allowing C5a to be assayed in normal plasma samples. Compsns. contg. MAb can be used to treat and prevent diseases associated with elevated C5a levels in the blood (esp. adult respiratory distress syndrome, sepsis, shock) or other disorders related to intra- or extra-vascular **complement** activation (e.g. rheumatic polyarthritis or lupus erythematosus). AIAb can be used to block reaction of C5a with its receptors.

2/10

L14 ANSWER 6 OF 8 WPIDS COPYRIGHT 1997 DERWENT INFORMATION LTD

AN 89-309498 [42] WPIDS

CR 91-132854 [18]; 93-175454 [21]

DNC C89-137014

TI New nucleic acid sequences encoding new CR1 protein - and its fragment, for diagnosis and control of **complement** related immune defects, inflammation, myocardial infarct, etc..

DC B04 D16

IN CARSON, G R; CONCINO, M F; FEARON, D T; IP, S H; KLINKSTEIN, L B; MAKRIDES, S C; MARSH, H C; WONG, W W

PA (BGHM) BRIGHAM & WOMENS HOSPITAL; (TCEL-N) T CELL SCI INC; (UYJO) UNIV JOHNS HOPKINS

CYC 20

PI WO 8909220 A 891005 (8942)* EN 191 pp

RW: AT BE CH DE FR GB IT LU NL SE

W: AU DK FI JP KR NO SU

ZA 8902397 A 891129 (9002)

AU 8935394 A 891016 (9008)

CN 1036987 A 891108 (9033)

ES 2014593 A 900716 (9033)

FI 9004842 A 901001 (9105)

EP 411031 A 910206 (9106)

R: AT BE CH DE FR GB IT LU NL SE

NO 9004213 A 901109 (9106)

DK 9002348 A 901130 (9113)

JP 04501502 W 920319 (9218) 59 pp
 AU 647371 B 940324 (9417)
 EP 411031 A4 920205 (9520)
 ADT WO 8909220 A WO 89-US1358 890331; ZA 8902397 A ZA 89-2397 890331; ES 2014593 A ES 89-112 890331; EP 411031 A EP 89-905249 890331; JP 04501502 W JP 89-505000 890331; AU 647371 B AU 89-35394 890331; EP 411031 A4 EP 89-905249 890331
 FDT AU 647371 B Previous Publ. AU 8935394, Based on WO 8909220
 PRAI US 88-176532 880401
 AB WO 8909220 A UPAB: 940622
 Nucleic acid sequences encoding a full-length CR1 protein (i.e. the C3b/C4b receptor) is new. The complete sequence over 6000 bases) is reproduced in the specification. Also new are (1) shortened forms of this sequence (specifically lacking the transmembrane region); (2) recombinant vectors and cells contg. such sequences, and (3) proteins (structures reproduced) and their fragments encoded by these sequences.
 Pref. the sequence may be DNA or RNA, and can be expressed in bacteria or mammalian cells.
 USE - The proteins (or their fragments) bind (3b and/or C4b; have I-cofactor activity and inhibit activity of C3 and C5 convertases. They are thus useful for treating immune disorders associated with **complement** activity; for preventing or treating damage caused by myocardial infarct or inflammation, and to prevent perfusion injury. The proteins derived **antibodies** and gene sequences can also be used to diagnose such conditions.
 Dwg.0/31

L14 ANSWER 7 OF 8 WPIDS COPYRIGHT 1997 DERWENT INFORMATION LTD
 AN 87-322653 [46] WPIDS
 DNN N87-241265 DNC C87-137507
 TI Mono clonal **antibodies** against C5A or DES-ARG74-C5A **complement** - used for treating injurious intravascular **complement** activation conditions or in diagnosis.
 DC B04 D16 S03
 IN DEINHART, T E; FENDLY, B M; LARRICK, J W
 PA (CETU) CETUS CORP; (CETU) CETUS ONCOLOGY CORP
 CYC 14
 PI EP 245993 A 871119 (8746)* EN 14 pp
 R: AT BE CH DE ES FR GB GR IT LI LU NL SE
 JP 62269699 A 871124 (8801)
 EP 245993 B1 930526 (9321) EN 18 pp
 R: AT BE CH DE ES FR GB GR IT LI LU NL SE
 DE 3785967 G 930701 (9327)
 ES 2054667 T3 940816 (9434)
 ADT EP 245993 A EP 87-303762 870428; JP 62269699 A JP 87-103396 870428; EP 245993 B1 EP 87-303762 870428; DE 3785967 G DE 87-3785967 870428; EP 87-303762 870428; ES 2054667 T3 EP 87-303762 870428
 FDT DE 3785967 G Based on EP 245993; ES 2054667 T3 Based on EP 245993
 PRAI US 86-856780 860428; US 86-947839 861230
 AB EP 245993 A UPAB: 930922
 A novel monoclonal **antibody** (MAb) binds with an affinity of at least 10 power 8 l/mole to human **complement** component C5a or des-arg74-C5a in the presence or absence of a molar excess of **complement** component C5 and blocks the binding of human C5a or human des-arg74-C5a to human granulocytes.
 USE - The **antibody** blocks the effect of C5a or des-arg74-C5a in vivo. It is used for prophylactically or therapeutically treating a patient for a condition associated with

injurious intravascular **complement** activation including patients receiving immunosuppressive therapy and those suffering from severe thermal burns or other serious injuries. Such conditions include Gram-negative sepsis, ARDS, thermal injury, pulmonary inflammation or injury, severe trauma, pancreatitis, myocardial infarction, massive blood transfusion, blood clots, cardiovascular disease, exposure to medical devices and/or acute phases of chronic autoimmune disease (including systemic lupus erythematosus and rheumatoid arthritis). The MABs may also be used immunologically or immunodiagnostically to detect the presence of human C5a or human des-arg74-C5a in fluids. The specificity of the MABs renders them useful for immunological studies of human C5a and its des-arg deriv., for affinity purifcn. of C5a or des-arg74-C5a and for neutralisation and/or removal of C5a or des-arg74-C5a from any reagents where it might be present.

0/0

L14 ANSWER 8 OF 8 WPIDS COPYRIGHT 1997 DERWENT INFORMATION LTD
 AN 84-006966 [02] WPIDS
 DNN N84-005116 DNC C84-002802
 TI Removal of **complement** components from biological fluids -
 by treatment with buffered acrinol to leave soln. for fragment
 assay.
 DC B04 K08 S03
 IN SATOH, P S
 PA (UPJO) UPJOHN CO
 CYC 12
 PI EP 97440 A 840104 (8402)* EN 14 pp
 R: BE CH DE FR GB IT LI NL SE
 JP 59005958 A 840112 (8408)
 FI 8302120 A 840131 (8411)
 CA 1202235 A 860325 (8617)
 EP 97440 B 860924 (8639) EN
 R: BE CH DE FR GB IT LI NL SE
 DE 3366421 G 861030 (8645)
 JP 04069345 B 921105 (9249) 6 pp
 ADT EP 97440 A EP 83-303142 830601; JP 59005958 A JP 83-104846 830610;
 JP 04069345 B JP 83-104846 830610
 FDT JP 04069345 B Based on JP 59005958
 PRAI US 82-388068 820614; US 83-518603 830729
 AB EP 97440 A UPAB: 930925

Removal of **complement** components C3, C4 and C5 from a biological fluid sample and recovery from the fluid of fragments C3a, C4a and C5a or their des-Arg derivs. is effected by adding an equal vol. of buffered 0.8-1.6% acrinol soln. to the sample, incubating the mixt. for 1 min.-2 hrs. at 25 deg.C and recovering the supernatant contg. the desired fragments.

In an assay for the fragments or their des-Arg derivs. the supernatant is then incubated with a known amount of **antibody** recognising the fragment or des-Arg deriv. The free labelled fragment is sepd. from the bound labelled fragment and the amount of labelled fragment in either material is measured. The results are compared with a standard curve.

The **complement** components are removed from biological samples, e.g. plasma, serum or urine, while fragments C3a, C4a and C5a and their des-Arg derivs. are recovered without interference with their immunogenicity. The fragments are anaphylatoxins and are involved in acute inflammatory processes, and so their assay is useful in medical diagnosis, esp. in the detection of autoimmune

Gambel 08/487,283

disorders and of iatrogenic **complement** activation.
0/0

=> fil biosis

FILE 'BIOSIS' ENTERED AT 09:58:09 ON 29 JUL 1997
COPYRIGHT (C) 1997 BIOSIS(R)

FILE COVERS 1969 TO DATE.
CAS REGISTRY NUMBERS AND CHEMICAL NAMES (CNs) PRESENT
FROM JANUARY 1969 TO DATE.

RECORDS LAST ADDED: 26 July 1997 (970726/ED)
CAS REGISTRY NUMBERS (R) LAST ADDED: 26 July 1997 (970726/UP)

=> d que l6;d his l7-

L1 737 SEA FILE=BIOSIS ABB=ON "EVANS M"/AU OR "EVANS M J"/AU
L2 138 SEA FILE=BIOSIS ABB=ON ("MATIS L"/AU OR "MATIS L A"/AU)

L3 666 SEA FILE=BIOSIS ABB=ON "MUELLER E"/AU OR "MUELLER E E"/A
U
L4 17 SEA FILE=BIOSIS ABB=ON ("NYE S"/AU OR "NYE S H"/AU)
L5 81 SEA FILE=BIOSIS ABB=ON ("ROLLINS S"/AU OR "ROLLINS S A"/
AU OR "ROLLINS S B"/AU OR "ROLLINS S D"/AU OR "ROLLINS S
L"/AU OR "ROLLINS S M"/AU OR "ROLLINS S R"/AU)
L6 1605 SEA FILE=BIOSIS ABB=ON L1 OR L2 OR L3 OR L4 OR L5

(FILE 'BIOSIS' ENTERED AT 09:55:17 ON 29 JUL 1997)

L7 1476 S COMPLEMENT AND C5
L8 14 S L7 AND L6
L9 10288 S ALPHA (2W) CHAIN#
L10 64 S L7 AND L9
L11 391924 S ANTIBOD? OR ANTI (2A) C5
L12 13 S L10 AND L11
~~L13 14 S L8 NOT L12]~~
L14 14 S L8 NOT L12

FILE 'BIOSIS' ENTERED AT 09:58:09 ON 29 JUL 1997

=> d bib ab l12 1-13;d bib ab l14 1-14

L12 ANSWER 1 OF 13 BIOSIS COPYRIGHT 1997 BIOSIS
AN 93:143342 BIOSIS
DN BA95:76142
TI MOLECULAR BASIS OF **COMPLEMENT** RESISTANCE OF HUMAN MELANOMA
CELLS EXPRESSING THE C3b-CLEAVING MEMBRANE PROTEASE P65.
AU OLLERT M W; KADLEC J V; PETRELLA E C; BREDEHORST R; VOGEL C-W
CS DEP. BIOCHEM. MOLECULAR BIOL., UNIV. HAMBURG, MARTIN-LUTHER-KING-PL.
6, 2000 HAMBURG 13, GER.
SO CANCER RES 53 (3). 1993. 592-599. CODEN: CNREA8 ISSN: 0008-5472
LA English
AB The molecular mechanism of **complement** resistance of the
human SK-MEL-170 melanoma cell line was investigated. The cells have
been shown to express the C3b-cleaving membrane protease p65. To
delineate the molecular consequences of the C3b-cleaving activity for
the **complement** cytotoxicity, the molecular events during
the initiation (R24 monoclonal **antibody**, C1), amplification

(C4, C3), and membrane attack (C5, C9) phases of **complement** were studied in comparison to a **complement**-susceptible human melanoma line (SK-MEL-93-2). No cleavage of C4b and C5b, 2 molecules structurally similar to C3b, was observed on the cells during classical pathway activation indicating the specificity of the p65 protease for the C3b molecule. The rapid degradation of C3b by p65 on the surface of **complement**-resistant SK-MEL-170 cells generates a Mr 30,000 C3.**alpha**.'-chain-fragment detectable as early as 1 min after **complement** activation, whereas no such fragment was present in detectable amounts on **complement**-susceptible cells. As a result of the rapid C3b proteolysis by p65 on resistant SK-MEL-170 cells, less C5 convertases are formed, which in turn results in the formation of a lower number of terminal **complement** components and membrane attack complexes. R24 antibody and Clq binding to the resistant cells was slightly lower as to susceptible cells. C4 binding studies, however, revealed that the observed difference in antibody and Clq binding has no influence on the **complement** resistance of SK-MEL-170 cells: significantly more C4b was bound to **complement**-resistant (1565 +/- 92 fg/cell) as compared to susceptible cells (715 +/- 31 fg/cell). On extraction of the molecular forms of C4 bound to the cell membranes, an additional high molecular weight C4 species-apparently a C4b-C4b homodimer-appeared only on the resistant SK-MEL-170 cells that may function as a residual back-up C5 convertase. Collectively, these results show that SK-MEL-170 human melanoma cells evade **complement**-mediated cytolysis despite sufficient activation of early components of the classical **complement** pathway by p65-mediated rapid degradation of surface-bound C3b, leading to a significant reduction in membrane attack complex formation. Thus, rapid cleavage of surface deposited C3b was established as a powerful mechanism of **complement** resistance.

L12 ANSWER 2 OF 13 BIOSIS COPYRIGHT 1997 BIOSIS

AN 92:477083 BIOSIS

DN BA94:108458

TI FORMATION AND STRUCTURE OF THE C5B-7 COMPLEX OF THE LYTIC PATHWAY OF **COMPLEMENT**.

AU DISCIPIO R G

CS DEP. IMMUNOLOGY IMM18, RESEARCH INSTITUTE SCRIPPS CLINIC, 10666 N. TORREY PINES RD., LA JOLLA, CALIF. 92037.

SO J BIOL CHEM 267 (24). 1992. 17087-17094. CODEN: JBCHA3 ISSN: 0021-9258

LA English

AB The formation and structure of the **complement** cytolytic intermediary complex, C5b-7, were studied with the aim of determining the interactive regions of C5, C6, and C7. The structure of human **complement** component C5 was elucidated by the application of limited proteolysis which generated well characterized major polypeptide fragments of this molecule. Plasmin, thrombin, and kallikrein cleave C5b with greater facility than C5. The most useful cleavage of C5b was effected by plasmin because the fragmentation pattern was similar to the processing the C3b by factors H, I, and kallikrein. Plasmin hydrolyzes peptide bonds within the .**alpha**.'-chain of C5b, resulting in a four-chain fragment, C5c (Mr = 142,000), and a single chain fragment, C5d (Mr = 43,000). Circular dichroism spectroscopic analyses indicated that C5d is substantially richer in .**alpha**.-helical content

than is C5c (27 versus 9%). Polyclonal **antibodies** directed against C5c blocked the interaction of C5b-6 with C7, whereas **antibodies** directed against C5d inhibited the binding of C5 with C3b. Chemical cross-linking using a cleavable radioiodinated photoreactive reagent revealed that both C6 and C7 associate preferentially with the **.alpha.'-chain** of C5b. The reversible interactions of C5 with C6, C7, and major polypeptide fragments derived from these were investigated with solid phase binding assays. The results indicate that the carboxyl-terminal domains of C6 and C7, which have cysteine-rich modules homologous to those found in factors H and I, have the capacity to link specifically with C5.

L12 ANSWER 3 OF 13 BIOSIS COPYRIGHT 1997 BIOSIS

AN 92:28069 BIOSIS

DN BA93:17344

TI AMINO ACID RESIDUES 1101-1105 OF THE ISOTYPIC REGION OF HUMAN C4B IS IMPORTANT TO THE COVALENT BINDING ACTIVITY OF **COMPLEMENT** COMPONENT C4.

AU REILLY B D; LEVINE R P; SKANES V M

CS FACULTY MEDICINE, MEMORIAL UNIVERSITY NEWFOUNDLAND, ST. JOHN'S, NFLD. CAN. A18 3V6.

SO J IMMUNOL 147 (9). 1991. 3018-3023. CODEN: JOIMA3 ISSN: 0022-1767

LA English

AB The C4A and C4B isotypes of human C4 show certain functional differences that stem from their relative preference for transacylation to amino (-NH₂) vs hydroxyl (-OH) nucleophiles, respectively, on **complement**-activating surfaces. Comparison of amino acid sequences of the **.alpha.-chain** fragment of C4, C4d, has shown C4A- and C4B-specific sequences at residues 1101-1106 are the only consistent structural difference between isotype, i.e., Pro, Cys, Pro, Val, Leu, Asp in C4A and Leu, Ser, Pro, Val, Ile, His in C4B. These residues may be responsible either in part or entirely for properties associated with isotype. To examine the functional role of residues 1101-1106 in C4B-mediated hemolysis, whole serum or immunopurified human C4 with allotypes, A3B1, A3, B2B1, or B1 were preincubated in the presence or absence of an antipeptide mAb (BII-1) specific for amino acid residues 1101-1105 of C4B. Sensitized sheep E and C4-deficient guinea pig serum was then added and lysis measured by absorbance at 415 nm. Our results show lysis of **antibody**-sensitized sheep E is inhibited by **antibody** and C4B2B1, C4B1, or C4A3B1 but not **antibody** and C4A3. The interference of hemolysis by BII-1 could not be explained by inhibition of activation of C4B or inhibition of C3 or C5 convertase activity. Furthermore, results from uptake experiments show that BII-1 interferes with the covalent binding activity of C4B, indicating residues 1101-1105 play a role in the covalent binding reaction of C4B to the target **E-antibody** complex.

L12 ANSWER 4 OF 13 BIOSIS COPYRIGHT 1997 BIOSIS

AN 91:409305 BIOSIS

DN BA92:76270

TI A COVALENT DIMER OF **COMPLEMENT** C4B SERVES AS A SUBUNIT OF A NOVEL C5 CONVERTASE THAT INVOLVES NO C3 DERIVATIVES.

AU MASAKI T; MATSUMOTO M; YASUDA R; LEVINE R P; KITAMURA H; SEYA T

CS DEP. IMMUNOLOGY, CENTER ADULT DISEASES, OSAKA, HIGASHINARI-KU, OSAKA 537, JPN.

SO J IMMUNOL 147 (3). 1991. 927-932. CODEN: JOIMA3 ISSN: 0022-1767

LA English

AB A C intermediate, LAC14, was prepared from TNP-aminocaproyl liposomes sensitized with anti-TNP **antibody** (Ab) and purified human C1 and C4. LAC14, containing radiolabeled C4, was analyzed by SDS-PAGE followed by autoradiography, and yielded a 210-kDa band and a predominant 400-kDa band. The 210-kDa band consisted of monomeric C4b bound to low molecular mass acceptors. The 400-kDa band was comprised of a 200-kDa moiety, as well as .beta.- and .gamma.-chains of C4. The 200-kDa moiety contained neither C1 nor sensitizing Ab, but it was largely decreased by treatment with NH₂OH to the 90-kDa moiety with the mobility corresponding to the .alpha.-**chain** of C4b. A covalent dimer of C4b, therefore, is the predominant form of C4b deposited on liposomes sensitized with **antibody**. The C4b-C4b dimer formed rapidly (within 5 min) followed by slow dissociation into monomers. The LAC14 bearing the C4b dimer but not the monomer was lysed, although with relatively low efficiency, by the addition of oxyC2 and EDTA-supplemented C3-deficient serum (C3DS), and, furthermore, LAC142 possessed the ability to convert **C5** into C5a and C5b. Moreover, lysis was inhibited not by anti-C3 Ab but by anti-C4 Ab. In other experiments, the dimer served as an element of C3 convertase, as well. These findings imply that the C4b dimer, when complexed with C2, expresses C3/C5 convertase activity without participation of C3, and may provide a molecular mechanism whereby sera from patients with complete C3 deficiency retain the ability to induce C-mediated cytolysis.

L12 ANSWER 5 OF 13 BIOSIS COPYRIGHT 1997 BIOSIS

AN 89:448305 BIOSIS

DN BA88:96577

TI RAPID ISOLATION AND CHARACTERIZATION OF NATIVE MOUSE

COMPLEMENT COMPONENTS C3 AND **C5**.

AU VAN DEN BERG C W; VAN DIJK H; CAPEL P J A

CS ACADEMIC HOSP. UTRECHT, LAB. MICROBIOL., POSTBUS 85500, 3508 GA UTRECHT, NETHERLANDS.

SO J IMMUNOL METHODS 122 (1). 1989. 73-78. CODEN: JIMMBG ISSN: 0022-1759

LA English

AB A rapid, 1 day procedure for the purification of mouse

complement factors C3 and **C5** is described. The method is based on fractionated precipitation by polyethylene glycol 6000, followed by MonoQ anion exchange chromatography on a system for fast protein liquid chromatography (FPLC). For C3 isolation, an additional FPLC separation step using Superose 12 (gel filtration) was used. C3 was purified 71-fold with a yield of 32% as measured by biological activity; the preparation contained no detectable contaminants as judged by SDS-PAGE. A comparable procedure for the isolation of **C5** resulted in a preparation with a considerable contamination which could be easily removed by affinity chromatography using **antibodies** directed against these contaminants. With this combined procedure **C5** was purified 536-fold with a yield of 28% based on biological activity. SDS-polyacrylamide gel electrophoresis revealed that mouse C3 and **C5** had apparent Mrs of 170,000 and 190,000, respectively. Under reducing conditions the .alpha. and .beta. **chains** showed Mrs of 107,000 and 62,000 for C3, and 104,000 and 85,000 for **C5**.

L12 ANSWER 6 OF 13 BIOSIS COPYRIGHT 1997 BIOSIS

AN 88:482712 BIOSIS

DN BA86:114022

TI ANALYSIS OF HUMAN C8 WITH MONOCLONAL **ANTIBODIES**
CHARACTERIZATION OF A MONOCLONAL **ANTIBODY** THAT RECOGNIZES
FREE C8-ALPHA-GAMMA SUBUNIT.

AU DOGLIO L T; GAWRYL M S; LINT T F

CS DEP. IMMUNOL./MICROBIOL., RUSH-PRESBYTERIAN-ST. LUKE'S MED. CENT.,
CHICAGO, ILLINOIS 60612.

SO J IMMUNOL 141 (6). 1988. 2079-2083. CODEN: JOIMA3 ISSN: 0022-1767

LA English

AB The eighth component of human C is essential for the formation of the
membranolytic C attack complex. C8 has a unique structure in that two
covalently linked chains, C8.alpha. and C8.gamma., are associated
non-covalently with the third chain, C8.beta.. In order to study the
structure and assembly of the C8 molecule, a panel of mAb has been
produced against the C component C8. Eight of these mAb had
reactivity to the C8.alpha.-.gamma. subunit, whereas four reacted
with C8.beta.. One of the C8.alpha.-.gamma. mAb, C8A2, had
specificity for an epitope on the C8.**alpha.-chain**
and exhibited no cross-reactivity to any of the other terminal C
components, including C8.beta.. C8A2 inhibited the hemolytic activity
of the C8.alpha.-.gamma. subunit but had no effect on the activity of
fluid phase whole C8 or C8 within membrane-bound C5b8. Functional
experiments suggest that C8A2 inhibits C8.alpha.-.gamma. activity by
interfering with its interaction with the C8.beta.-chain. In an
enzyme immunoassay using the C8A2 mAb, free C8.alpha.-.gamma. subunit
could be detected in both homozygous and heterozygous
C8.beta.-deficient serum. However, only low level binding was
observed when homozygous C5- and C7-deficient sera were
tested. Thus the mAb, C8A2, recognizes an epitope expressed on the
C8.alpha.-.gamma. subunit but not on intact C8 and can detect free
C8.alpha.-.gamma. in the presence of native C8.

L12 ANSWER 7 OF 13 BIOSIS COPYRIGHT 1997 BIOSIS

AN 88:331418 BIOSIS

DN BA86:37969

TI USE OF ANTISERA TO THE ISOLATED ALPHA AND BETA SUBUNITS OF C3 AS
PROBES TO STUDY FUNCTIONAL SITES PRESENT ON PARTICLE-BOUND C3B BUT
ABSENT ON NATIVE SOLUBLE FORMS OF C3.

AU WHALEY K; NILSSON U

CS BLOOD CENTRE, UNIV. HOSP., S-751 85 UPPSALA, SWEDEN.

SO INT ARCH ALLERGY APPL IMMUNOL 86 (1). 1988. 55-61. CODEN: IAAAAM
ISSN: 0020-5915

LA English

AB The effect of antisera to the isolated **.alpha.** and **.beta.**
chains of C3 on certain C3b-dependent reactions has been
studied. C5-mediated haemolysis of EAC1423b was inhibited
preferentially by antiserum to the **.alpha. chain**,
whereas antiserum to the **.beta. chain** inhibited the formation of
C3bBb. The anti-.beta. chain antiserum also stabilised C3bBbP, and
rendered the enzyme relatively resistant to accelerated decay in the
presence of factor H. These and previous findings that anti-.alpha.
and anti-.beta. IgG bind to restricted subsets of antigenic
determinants on C3/C3b suggest that these antisera affect C3b
function through the binding of **antibodies** to active
binding sites exclusively exposed by bound C3b. The anti-.alpha. and
anti-.beta. **antibody** probes are currently being further
developed to verify this interpretation.

L12 ANSWER 8 OF 13 BIOSIS COPYRIGHT 1997 BIOSIS

AN 87:359289 BIOSIS

DN BA84:56692

TI TRYPANOSOMA-LEWISI RESTRICTION OF ALTERNATIVE **COMPLEMENT** PATHWAY C3-C5 CONVERTASE ACTIVITY.

AU STURTEVANT J E; BALBER A E

CS DIV. IMMUNOL., DEP. MICROBIOL. AND IMMUNOL., DUKE UNIVERSITY MED. CENT., P.O. BOX 3010, DURHAM, N.C. 27710, USA.

SO EXP PARASITOL 63 (3). 1987. 260-271. CODEN: EXPAAA ISSN: 0014-4894

LA English

AB The rat parasite Trypanosoma lewisi was incubated in vitro with rat or human serum, washed, and extracted in detergent. Extracts were fractionated by electrophoresis in denaturing gels, transferred to nitrocellulose, allowed to renature, then immunoblotted with polyclonal **antibodies** to rat **complement** component C3 and human **complement** components C3, C5, and factor B. Molecules that reacted with these **antibodies** were detected in the extracts. Fragments of rat C3 were detected in extracts of parasites that had not been exposed to serum in vitro. Additional **complement** deposition occurred during in vitro incubations; human **complement** components deposited in vitro could be distinguished from rat components deposited in vivo. **Complement** deposition in vitro required magnesium ions and did not occur when heat inactivated serum was used. Components reacting with **antibodies** to human C3 included a group of bands with molecular weights higher than C3.alpha. or .beta. **chains**. Blotting with affinity purified, chain specific **antibodies** demonstrated that a 68 kDa component on parasites is C3.beta. and that a 44 kDa molecule is derived from C3.alpha.. A 73 kDa component that was difficult to resolve from C3.beta. is probably also a C3.alpha. fragment. This suggests that an inactive iC3b-like molecule is present on parasites. Kinetic studies showed that cleavage of C3.alpha. is rapid and that the amount of C3.alpha. fragments and C3.beta. on intact parasites reached a steady state after 15 min. When parasites were trypsinized prior to incubation in C5 or C6 deficient serum, the rate and extent of C3 and C5 deposition increased. Unprocessed C3.alpha.' and C5.alpha.' **chains** were detected. Trypsinized parasites were lysed by the alternative **complement** pathway in normal serum. Intact parasites could be lysed by **complement** in the presence of **antibody**. The data support our previous suggestion that trypsin sensitive surface proteins on intact T. lewisi limit alternative pathway activity by restricting C3/C5 convertase activity.

L12 ANSWER 9 OF 13 BIOSIS COPYRIGHT 1997 BIOSIS

AN 87:337772 BIOSIS

DN BA84:46715

TI FUNCTIONAL ANALYSIS AND QUANTIFICATION OF THE **COMPLEMENT** C3 DERIVED ANAPHYLATOXIN C3A WITH A MONOCLONAL **ANTIBODY**.

AU BURGER R; BADER A; KIRSCHFINK M; ROTHER U; SCHROD L; WOERNER I; ZILOW G

CS INST. IMMUNOL., IM NEUENHEIMER FELD 305, 6900 HEIDELBERG, W. GER.

SO CLIN EXP IMMUNOL 68 (3). 1987. 703-711. CODEN: CEXIAL ISSN: 0009-9104

LA English

AB The C3 fragment C3a belongs to the anaphylatoxins. It has immune regulatory activity and contributes to the pathogenesis of the adult respiratory distress syndrome (ARDS). The low molecular weight (9 kD)

of C3a complicates the production of **antibodies** to C3a. We obtained a monoclonal **antibody** (designated H13) to human C3a. It reacts with C3a or C3a-desArg and with native C3 but not with C5 or C5a. In immunoblot analysis it reacts with the .alpha.- but not with .beta.-chain of C3 and binds to a protein with a mol. wt of about 10 kD present in zymosan-activated sera which is only marginally detectable in non-activated serum and absent in plasma. H13 crossreacts with the analogous proteins of rabbit, guinea pig and sheep. H13 has the capacity to bind 125I-radiolabelled C3a efficiently but fails totally to react with 125I-C5a or with other C3 .alpha.-chain fragments, H13 blocks C3a functional activity. It markedly inhibits C3a-induced 3H-serotonin release from platelets in vitro and similarly inhibits the C3a-induced extravasation of Evans blue into the skin in vivo. H13 does not interfere with the haemolytic activity of C3. An ELISA system was established using H13 which permits quantification of C3a in sera of polytrauma patients. The **antibody** H13 should facilitate further functional analysis of C3a in experimental systems. It should be useful for quantification of C3a in diagnostic assays and also for application in immunopathology.

L12 ANSWER 10 OF 13 BIOSIS COPYRIGHT 1997 BIOSIS

AN 87:337585 BIOSIS

DN BA84:46528

TI COVALENT ASSOCIATION OF C3B WITH C4B WITHIN C5 CONVERTASE OF THE CLASSICAL **COMPLEMENT** PATHWAY.

AU TAKATA Y; KINOSHITA T; KOZONO H; TAKEDA J; TANAKA E; HONG K; INOUE K

CS DEP. BACTERIOLOGY, OSAKA UNIV. MED. SCH., SUITA, OSAKA 565, JAPAN.

SO J EXP MED 165 (6). 1987. 1494-1507. CODEN: JEMEA V ISSN: 0022-1007

LA English

AB The C convertase of the classical **complement** pathway is a complex enzyme consisting of three **complement** fragments, C4b, C2a, and C3b. Previous studies have elucidated functional roles of each subunit (4, 6, 7), but, little is known about how the subunits associate with each other. In this investigation, we studied the nature of the classical C% convertase that was assembled on sheep erythrocytes. We found that one of the nascent C3b molecule that had been generated by the C3 convertase directly bound covalently to C4b. C3b bound to the .alpha.' chain of C4b through an ester bond, which could be cleaved by treatment with hydroxylamine. The ester bond was rather unstable, with a half-life of 7.9 h at pH 7.4 and 37% C. Formation of the C4b-C3b dimer is quite efficient; e.g., 54% of the cell-bound C3b was associated with C4b when 25,000 molecules of C4b and 12,000 molecules of C3b were present per cell. Kinetic analysis also showed the efficient formation of the C4b-C3b dimer; the rate of dimer formation was similar to or even faster than that of cell-bound monomeric C3b molecules. These results indicate that the C4b is a highly reactive acceptor molecule for nascent C3b. High-affinity C5-binding site with an association constant of 2.1 .times. 10⁸ L/M were demonstrated on C4b-C3b dimer-bearing sheep erythrocytes, EAC43 cells. The number of high-affinity C5-binding sites coincided with the number of C4b-C3b dimers, but not with the total number of cell-bound C3b molecules. Anti-C4 **antibodies** caused 80% inhibition of the binding of C5 to EAC43 cells. These results suggest that only C4b-associated C3b serves as a high-affinity C5 binding site. EAC14 cells had a small amount of high-affinity C5 binding sites with an association constant of 8.1 .times. 10⁷ L/M 100 molecules of bound C4b being necessary for 1 binding

site. In accordance with the hypothesis that C4b-associated C4b might also serve as a high-affinity C5-binding site, a small amount of C4b-C4b dimer was detected on EAC14 cells by SDS-PAE analysis. Taken together, these observations indicate that high-affinity binding of C5 is probably divalent, in that C5 recognizes both promoters with dimers. The high-affinity binding may allow selective binding of C5 to the convertase in spite of surrounding monomeric C3b molecules.

L12 ANSWER 11 OF 13 BIOSIS COPYRIGHT 1997 BIOSIS

AN 84:339305 BIOSIS

DN BA78:75785

TI RESIDUAL HEMOLYTIC AND PROTEOLYTIC ACTIVITY EXPRESSED BY BB AFTER DECAY DISSOCIATION OF C-3B BB.

AU FISHELSON Z; MULLER-EBERHARD H J

CS DEPARTMENT OF IMMUNOLOGY, RESEARCH INSTITUTE OF SCRIPPS CLINIC, LA JOLLA, CALIF. 92037.

SO J IMMUNOL 132 (3). 1984. 1425-1429. CODEN: JOIMA3 ISSN: 0022-1767
LA English

AB Bb [factor B, fragment b] (MW = 63,000) is the catalytic site-bearing subunit of the C3 [complement component 3] convertase of the alternative complement pathway, C3b,Bb, which is dissociated from the complex upon decay of the enzyme. Because purified Bb induced certain leukocyte activities, it was examined whether it expresses residual hemolytic or proteolytic activity. Hemolytic activity of Bb was tested by using Factor B- or Factor D-depleted normal human serum and rabbit or sheep erythrocytes. Proteolytic activity of Bb was assessed by using purified C3 or C5 as substrates and SDS-PAGE [sodium dodecyl sulfate-polyacrylamide gel electrophoresis] to detect protein cleavage. Bb expressed metal-dependent hemolytic activity that was .apprx. 100-fold lower than that of Factor B. This activity could be inhibited by Factor H and enhanced by properdin. Low but statistically significant binding of 125I-labeled Bb to C3b on erythrocytes was demonstrated. Monoclonal antibodies that bind to Bb but not to intact Factor B inhibited the Bb hemolytic activity. Purified Bb cleaved C3 to C3a and C3b, as evidenced by the appearance of the .alpha.'-chain of C3b. It also cleaved C5 to C5a and C5b when cobra venom factor [CVF] was present in the reaction mixture. Metal ions were required for expression of proteolytic activity, and Ni supported the activity better than Mg. Decayed Bb has residual C3 and C5 cleaving activity and hemolytic activity, expression of which appears to require its association with C3b, C3(H2O), or CVF. These observations may aid in explaining the mechanism of action of Bb on leukocytes.

L12 ANSWER 12 OF 13 BIOSIS COPYRIGHT 1997 BIOSIS

AN 82:150280 BIOSIS

DN BA73:10264

TI COMPLEMENT RECEPTOR IS AN INHIBITOR OF THE COMPLEMENT CASCADE.

AU IIDA K; NUSSENZWEIG V

CS DEP. PATHOL., N.Y. MED. CENT., NEW YORK, 10016, USA.

SO J EXP MED 153 (5). 1981. 1138-1150. CODEN: JEMEA V ISSN: 0022-1007
LA English

AB A glycoprotein from the membrane of human erythrocytes was identified as a receptor for C3b (b fragment of complement component 3) (CR1). It promotes the dissociation of the alternative pathway C3 convertase C3b,Bb and the cleavage of C3b by C3b/C4b inactivator. CR1

also inactivates the C3 and C5 convertases of the classical pathway. CR1 inhibits the consumption of C3 by C3 convertase EAC142 (sheep erythrocyte-antibody-complement complex) and enhances the decay of C4b,2a sites. On a weight basis, CR1 is 5-10 times more active than C4 binding protein, a serum inhibitor of C4b,2a. The binding of 125I-CR1 to EAC14 cells is inhibited by C2. CR1 and C2 probably compete for a site on C4b. CR1 inhibited C5 convertase even more effectively, but had no effect on the assembly of the late complement components. At high concentrations, CR1 alone has no irreversible effects on cell-bound C4b. In the fluid phase, CR1 can function as a cofactor for the cleavage of the .alpha.' chain of C4b by C3b/C4b inactivator. A well-known function of CR1 is to promote adherence of microbes or immune complexes bearing C3b and C4b to cells. This interaction could result in a microenvironment damaging to the plasma membrane of the responding cell because the extrinsic C3b and C4b fragments can serve as additional sites of assembly of enzymes of the cascade. CR1 on the surface of cells may supply an increased local concentration of a strong inhibitor of the amplifying enzymes of the complement system and may provide cells with a mechanism for circumventing damage when they bind C3b- and C4b-bearing substrates.

L12 ANSWER 13 OF 13 BIOSIS COPYRIGHT 1997 BIOSIS

AN 80:162533 BIOSIS

DN BA69:37529

TI BIOSYNTHESIS OF A SINGLE CHAIN PRO COMPLEMENT C-5 BY NORMAL MOUSE LIVER MESSENGER RNA ANALYSIS OF THE MOLECULAR BASIS OF

COMPLEMENT C-5 DEFICIENCY IN AKR-J MICE.

AU PATEL F; MINTA J O

CS DEP. PATHOL., UNIV. TORONTO, TORONTO, ONT. M5S 1A8, CAN.

SO J IMMUNOL 123 (5). 1979. 2408-2414. CODEN: JOIMA3 ISSN: 0022-1767

LA English

AB An in vivo labeling technique was used to prove the molecular lesions precipitating in C5 [complement component 5] deficiency in the AKR/J mouse. 14C-labeled amino acids were administered i.p. into normal and C5-deficient mice and the plasma was harvested 4 h later. By using monospecific anti-C5, newly synthesized 14C-C5 was immunoprecipitated from the plasma and postmitochondrial supernatants (PMS) of a liver homogenate. SDS-PAGE [sodium dodecyl sulfate-polyacrylamide gel electrophoresis] analysis demonstrated that normal mouse plasma (apparent MW 205,000) was composed of 2 dissimilar subunits, an .alpha.-chain (115,000 daltons) and a .beta.-chain (82,000). Nonsecreted C5 immunoprecipitated from the PMS was resolved into 2 nonreducible polypeptide chains of MW 200,000 and 170,000 respectively. By comparison to plasma C5, the 170,000 dalton peak polypeptide chain probably represents incompletely synthesized, partially degraded or unglycosylated pro-C5. 14C-C5 immunoprecipitates from the plasma and the PMS of AKR/J C5-deficient mice contained insignificant radioactivity and on SDS gels did not resolve into any distinct peaks, suggesting that C5 is not synthesized in this strain. 14C-C3 immunoprecipitated from the plasma of normal and AKR/J mice in each case was composed of covalently-linked .alpha.- and .beta.-chains (MW 130,000 and 85,000, respectively). 14C-C3 immunoprecipitated from the PMS of normal and C5-deficient liver homogenates in each case migrated on SDS gels as a single polypeptide chain, pro-C3 (MW 200,000). These findings were confirmed by cell-free translation studies. Poly(A)-mRNA isolated

from normal mouse liver stimulated the incorporation of 3H-leucine into protein in a time-dependent fashion in a reticulocyte lysate system [rabbit] under optimal conditions. 3H-C5 immunoprecipitated from the translation reaction mixture behaved as a single nonreducible polypeptide chain (MW 170,000). Poly A-mRNA from the liver of the AKR/J mouse displayed similar kinetics and dose-response stimulation of protein synthesis upon translation in the cell-free system, but failed to direct the synthesis of C5 or C5 immunoreactive peptides, although C3 was synthesized normally as pro-C3. Since the intact machinery for carbohydrate synthesis is not present in the reticulocyte cell-free system, the 170,000-dalton C5 polypeptide chain is possibly unglycosylated pro-C5. Thus, C5 is synthesized as a single-chain pro-C5 and post-translationally converted to a two-subunit C5 molecule by limited proteolysis. In the AKR/J C5-deficient mouse C5 is not synthesized at all, suggesting the lack of a functional mRNA for C5 in this strain.

L14 ANSWER 1 OF 14 BIOSIS COPYRIGHT 1997 BIOSIS

AN 97:296290 BIOSIS

DN 99595493

TI Inhibition of **complement** activity by humanized anti-C5 antibody and single-chain Fv.

AU Thomas T C; Rollins S A; Rother R P; Giannoni M A; Hartman S L; Elliott E A; Nye S H; Matis L A; Squinto S P; Evans M J

CS Alexion Pharmaceuticals, 25 Science Park, New Haven, CT 06511, USA

SO Molecular Immunology 33 (17-18). 1996 (1997). 1389-1401. ISSN: 0161-5890

LA English

AB Activation of the **complement** system contributes significantly to the pathogenesis of numerous acute and chronic diseases. Recently, a monoclonal antibody (5G1.1) that recognizes the human **complement** protein C5, has been shown to effectively block C5 cleavage, thereby preventing the generation of the pro-inflammatory **complement** components C5a and C5b-9. Humanized 5G1.1 antibody, Fab and scFv molecules have been produced by grafting the complementarity determining regions of 5G1.1 on to human framework regions. Competitive ELISA analysis indicated that no framework changes were required in the humanized variable regions for retention of high affinity binding to C5, even at framework positions predicted by computer modeling to influence CDR canonical structure. The humanized Fab and scFv molecules blocked **complement**-mediated lysis of chicken erythrocytes and porcine aortic endothelial cells in a dose-dependent fashion, with complete **complement** inhibition occurring at a three-fold molar excess, relative to the human C5 concentration. In contrast to a previously characterized anti-C5 scFv molecule, the humanized h5G1.1 scFv also effectively blocked C5a generation. Finally, an intact humanized h5G1.1 antibody blocked human **complement** lytic activity at concentrations identical to the original murine monoclonal antibody. These results demonstrate that humanized h5G1.1 and its recombinant derivatives retain both the affinity and blocking functions of the murine 5G1.1 antibody, and suggest that these molecules may serve as potent inhibitors of **complement**-mediated pathology in human

inflammatory diseases.

L14 ANSWER 2 OF 14 BIOSIS COPYRIGHT 1997 BIOSIS

AN 97:147682 BIOSIS

DN 99446885

TI Monoclonal antibody to **C5** inhibits C5a and C5b-9 generation without inhibition of C3 cleavage and significantly limits myocardial ischemia and reperfusion induced tissue damage.

AU Vakeva A; **Rollins S A**; **Matis L A**; Stahl G L

CS Brigham Women's Hosp., Boston, MA, USA

SO 46th Annual Scientific Session of the American College of Cardiology, Anaheim, California, USA, March 16-19, 1997. Journal of the American College of Cardiology 29 (2 SUPPL. A). 1997. 267A. ISSN: 0735-1097

DT Conference

LA English

L14 ANSWER 3 OF 14 BIOSIS COPYRIGHT 1997 BIOSIS

AN 96:501911 BIOSIS

DN 99224267

TI Subcutaneous administration of anti-**C5** monoclonal antibody induces systemic **complement** inhibition and ameliorates immune complex mediated inflammatory responses.

AU Wang Yi; Hu Q; Kristan J; **Rollins S**; **Evans M**; Madri J; **Matis L**

CS Alexion Pharm. Inc., 25 Science Park, New Haven, CT 06511, USA

SO 60th National Scientific Meeting of the American College of Rheumatology and the 31st National Scientific Meeting of the Association of Rheumatology Health Professionals, Orlando, Florida, USA, October 18-22, 1996. Arthritis & Rheumatism 39 (9 SUPPL.). 1996. S245. ISSN: 0004-3591

DT Conference

LA English

L14 ANSWER 4 OF 14 BIOSIS COPYRIGHT 1997 BIOSIS

AN 96:413396 BIOSIS

DN 99135752

TI Amelioration of lupus-like autoimmune disease in NZB-W F-1 mice after treatment with a blocking monoclonal antibody specific for **complement** component **C5**.

AU Wang Yi; Hu Q; Madri J A; **Rollins S A**; Chodera A; **Matis L A**

CS Immunobiol. Program, Alexion Pharmaceuticals, Inc., New Haven, CT 06511, USA

SO Proceedings of the National Academy of Sciences of the United States of America 93 (16). 1996. 8563-8568. ISSN: 0027-8424

LA English

AB New Zealand black times New Zealand white (NZB/W) F-1 mice spontaneously develop an autoimmune syndrome with notable similarities to human systemic lupus erythematosus. Female NZB/W F-1 mice produce high titers of antinuclear antibodies and invariably succumb to severe glomerulonephritis by 12 months of age. Although the development of the immune-complex nephritis is accompanied by abundant local and systemic **complement** activation, the role of proinflammatory **complement** components in disease progression has not been established. In this study we have examined the contribution of activated terminal **complement** proteins to the pathogenesis of the lupus-like autoimmune disease. Female NZB/W F-1 mice were treated with a monoclonal antibody (mAb) specific for the **C5** component of **complement** that blocks

the cleavage of **C5** and thus prevents the generation of the potent proinflammatory factors C5a and C5b-9. Continuous therapy with anti-C5 mAb for 6 months resulted in significant amelioration of the course of glomerulonephritis and in markedly increased survival. These findings demonstrate an important role for the terminal **complement** cascade in the progression of renal disease in NZB//W F-1 mice, and suggest that mAb-mediated **C5** inhibition may be a useful approach to the therapy of immune-complex glomerulonephritis in humans.

L14 ANSWER 5 OF 14 BIOSIS COPYRIGHT 1997 BIOSIS

AN 96:107988 BIOSIS

DN 98680123

TI In vitro and in vivo inhibition of **complement** activity by a single-chain Fv fragment recognizing human **C5**.

AU Evans M J; Rollins S A; Wolff D W; Rother R P; Norin A J; Therrien D M; Grijalva G A; Mueller J P; Nye S H; Squinto S P; Wilkins J A

CS Dep. Molecular Dev., Alexion Pharmaceuticals, 25 Science Park, New Haven, CT 06511, USA

SO Molecular Immunology 32 (16). 1995. 1183-1195. ISSN: 0161-5890

LA English

AB **Complement** activation has been implicated in the pathogenesis of several human diseases. Recently, a monoclonal antibody (N19-8) that recognizes the human **complement** protein **C5** has been shown to effectively block the cleavage of **C5** into C5a and C5b, thereby blocking terminal **complement** activation. In this study, a recombinant N19-8 scFv antibody fragment was constructed from the N19-8 variable regions, and produced in both mammalian and bacterial cells. The N19-8 scFv bound human **C5** and was as potent as the N19-8 monoclonal antibody at inhibiting human C5b-9-mediated hemolysis of chicken erythrocytes. In contrast, the N19-8 scFv only partially retained the ability of the N19-8 monoclonal antibody to inhibit C5a generation. To investigate the ability of the N19-8 scFv to inhibit **complement**-mediated tissue damage, **complement**-dependent myocardial injury was induced in isolated mouse hearts by perfusion with Krebs-Henseleit buffer containing 6% human plasma. The perfused hearts sustained extensive deposition of human C3 and C5b-9, resulting in increased coronary artery perfusion pressure, end-diastolic pressure, and a decrease in heart rate until the hearts ceased beating approximately 10 min after the addition of plasma. Hearts treated with human plasma supplemented with either the N19-8 monoclonal antibody or the N19-8 scFv did not show any detectable changes in cardiac performance for at least 1 hr following the addition of plasma. Hearts treated with human plasma alone showed extensive deposition of C3 and C5b-9, while hearts treated with human plasma containing the N19-8 scFv showed extensive deposition of C3, but no detectable deposition of C5b-9. Administration of a 100 mg bolus dose of N19-8 scFv to rhesus monkeys inhibited the serum hemolytic activity by at least 50% for up to 2 hr. Pharmacokinetic analysis of N19-8 scFv serum levels suggested a two-compartment model with a T-1/2-alpha of 27 min. Together, these data suggest the recombinant N19-8 scFv is a potent inhibitor of the terminal **complement** cascade and may have potential in vivo applications where short duration inhibition of terminal **complement** activity is desirable.

L14 ANSWER 6 OF 14 BIOSIS COPYRIGHT 1997 BIOSIS

AN 96:61239 BIOSIS

DN 98633374

TI Monoclonal antibodies directed against human **C5** and **C8** block **complement**-mediated damage of xenogeneic cells and organs.

AU **Rollins S A**; **Matis L A**; Springhorn J P; Setter E; Wolff D W

CS Dep. Immunol., Alexion Pharmaceutical Inc., 25 Science Park, New Haven, CT 06511, USA

SO Transplantation (Baltimore) 60 (11). 1995. 1284-1292. ISSN: 0041-1337

LA English

AB The hyperacute rejection (HAR) of xenotransplanted organs is initiated by the deposition of natural antibodies on donor endothelium followed by the activation of the recipient **complement** system, which rapidly destroys the graft. Studies of the role of activated **complement** in HAR have suggested that natural antibody as well as early (**C3a**, **C3b**) and late (**C5a**, **C5b-9**) activated **complement** components may contribute to cell activation and damage. Attenuation of HAR has been achieved by blockade of **C3** activation with soluble **CR1** or consumptive depletion of **complement** with cobra venom factor; however, similar studies using specific inhibitors of terminal **complement** components have not been described. To address the contribution of **C5a** and the membrane attack complex (**C5b-9**, **MAC**) to **complement**-mediated xenogeneic cell and organ damage, we utilized functionally blocking monoclonal antibodies directed against the human terminal **complement** components **C5** and **C8**. Our data show that both anti-**C5** and anti-**C8** mAbs protect porcine aortic endothelial cells from membrane damage mediated by human **C5b-9**. Additionally, both the anti-**C5** and anti-**C8** mAbs blocked **complement**-mediated generation of membrane prothrombinase activity on porcine aortic endothelial cells challenged with human serum. To test the ability of these antibodies to attenuate antibody and **complement**-mediated damage of xenogeneic organs, an ex vivo model was developed wherein isolated rat hearts were perfused with human serum in the presence or absence of the anti-**C5** and anti-**C8** mAbs. Our data demonstrate that mAbs directed against human **C5** and **C8** prevented organ damage by human serum **complement** and suggest that these molecules may serve as potent inhibitors of HAR.

L14 ANSWER 7 OF 14 BIOSIS COPYRIGHT 1997 BIOSIS

AN 96:61228 BIOSIS

DN 98633363

TI **Complement** inhibition with an anti-**C5** monoclonal antibody prevents acute cardiac tissue injury in an ex vivo model of pig-to-human xenotransplantation.

AU Kroshus T J; **Rollins S A**; Dalmasso A P; Elliott E A;

Matis L A; Squinto S P; Bolman R M III

CS Dep. Surgery, Univ. Minn., Box 207, UMHC, 420 Delaware St. SE, Minneapolis, MN 55455, USA

SO Transplantation (Baltimore) 60 (11). 1995. 1194-1202. ISSN: 0041-1337

LA English

AB Prevention of hyperacute xenograft rejection in the pig-to-primate combination has been accomplished by removal of natural antibodies, **complement** depletion with cobra venom factor, or prevention of **C3** activation with the soluble **complement** inhibitor

sCR1. Although these strategies effectively prevent hyperacute rejection, they do not address the relative contribution of early (C3a, C3b) versus late (C5a, C5b-9) activated **complement** components to xenogeneic organ damage. To better understand the role of the terminal **complement** components (C5a, C5b-9) in hyperacute rejection, an anti-human C5 mAb was developed and tested in an ex vivo model of cardiac xenograft rejection. In vitro studies demonstrated that the anti-C5 mAb effectively blocked C5 cleavage in a dose-dependent manner that resulted in complete inhibition of both C5a and C5b-9 generation. Addition of anti-C5 mAb to human blood used to perfuse a porcine heart prolonged normal sinus cardiac rhythm from a mean time of 25.2 min in hearts perfused with unmodified blood to 79,296, or gt 360 min when anti-C5 mAb was added to the blood at 50 mu-g/ml, 100 mu-g/ml, or 200 mu-g/ml, respectively. In these experiments, activation of the classical **complement** pathway was completely inhibited. Hearts perfused with blood containing the highest concentration of anti-C5 mAb had no histologic evidence of hyperacute rejection and no deposition of C5b-9. These experiments suggest that the activated terminal **complement** components C5a and C5b-9, but not C3a or C3b, play a major role in tissue damage in this porcine-to-human model of hyperacute rejection. They also suggest that targeted inhibition of terminal **complement** activation by anti-C5 mAbs may be useful in clinical xenotransplantation.

L14 ANSWER 8 OF 14 BIOSIS COPYRIGHT 1997 BIOSIS

AN 95:549139 BIOSIS

DN 98563439

TI A novel bifunctional chimeric **complement** inhibitor that regulates C3 convertase and formation of the membrane attack complex.

AU Fodor W L; Rollins S A; Guilmette E R; Setter E; Squinto S P

CS Alexion Pharmaceuticals Inc., 25 Science Park, Suite 360, New Haven, CT 06511, USA

SO Journal of Immunology 155 (9). 1995. 4135-4138. ISSN: 0022-1767

LA English

AB Human cells express cell surface **complement** regulatory molecules that inhibit the activity of the C3/C5 convertases (DAF, MCP, CR1) or inhibit the membrane attack complex (CD59). A single molecule that inhibits both the convertase activity and formation of the membrane attack complex has never been characterized. To this end, we have developed two reciprocal chimeric **complement** inhibitors (CD, NH2-CD59-DAF-GPI; and DC, NH2-DAF-CD59-GPI) that contain the functional domains of decay accelerating factor (DAF; CD55) and CD59. Cell surface expression of the CD and DC chimeric proteins was detected with DAF- and CD59-specific antisera. Cell surface C3d deposition was inhibited on cells expressing the chimeric molecules, thereby indicating that the DAF moiety was functional in both molecules. Conversely, Ab-blocking experiments demonstrated that only the DC molecule retained CD59 function. Therefore, the DC molecule represents a novel potent chimeric bifunctional **complement** inhibitor that retains the functional domains of two distinct **complement** regulatory molecules.

L14 ANSWER 9 OF 14 BIOSIS COPYRIGHT 1997 BIOSIS

AN 95:521823 BIOSIS

DN 98536123

TI Anti-C5 monoclonal antibody therapy prevents collagen-induced arthritis and ameliorates established disease.
 AU Wang Y; **Rollins S**; Madri J; **Matis L**
 CS Alexion Pharmaceutical Inc., 25 Science Park, New Haven, CT 06511, USA
 SO 59th National Scientific Meeting of the American College of Rheumatology and the 30th National Scientific Meeting of the Association of Rheumatology Health Professionals, San Francisco, California, USA, October 21-26, 1995. Arthritis & Rheumatism 38 (9 SUPPL.). 1995. S372. ISSN: 0004-3591
 DT Conference
 LA English

L14 ANSWER 10 OF 14 BIOSIS COPYRIGHT 1997 BIOSIS

AN 95:511655 BIOSIS

DN 98516705

TI Anti-C5 monoclonal antibody therapy prevents collagen-induced arthritis and ameliorates established disease.

AU Wang Y; **Rollins S A**; Madri J A; **Matis L A**

CS Immunobiol. Program, Alexion Pharm. Inc., New Haven, CT 06511, USA

SO Proceedings of the National Academy of Sciences of the United States of America 92 (19). 1995. 8955-8959. ISSN: 0027-8424

LA English

AB Activated components of the **complement** system are potent mediators of inflammation that may play an important role in numerous disease states. For example, they have been implicated in the pathogenesis of inflammatory joint diseases including rheumatoid arthritis (RA). To target **complement** activation in immune-mediated joint inflammation, we have utilized monoclonal antibodies (mAbs) that inhibit the **complement** cascade at C5, blocking the generation of the major chemotactic and proinflammatory factors C5a and C5b-9. In this study, we demonstrate the efficacy of a mAb specific for murine C5 in the treatment of collagen-induced arthritis, an animal model for RA. We show that systemic administration of the anti-C5 mAb effectively inhibits terminal **complement** activation in vivo and prevents the onset of arthritis in immunized animals. Most important, anti-C5 mAb treatment is also highly effective in ameliorating established disease. These results demonstrate a critical role for activated terminal **complement** components not only in the induction but also in the progression of collagen-induced arthritis and suggest that C5 may be an attractive therapeutic target in RA.

L14 ANSWER 11 OF 14 BIOSIS COPYRIGHT 1997 BIOSIS

AN 95:479674 BIOSIS

DN 98493974

TI Blockade of C5a and C5b-9 generation inhibits leukocyte and platelet activation during extracorporeal circulation.

AU Rinder C S; Rinder H M; Smith B R; Fitch J C K; Smith M J; Tracey J B; **Matis L A**; Squinto S P; **Rollins S A**

CS Dep. Anesthesiol., Tompkins 3, Yale Univ. Sch. Med., 333 Cedar St., New Haven, CT 06510, USA

SO Journal of Clinical Investigation 96 (3). 1995. 1564-1572. ISSN: 0021-9738

LA English

AB **Complement** activation contributes to the systemic inflammatory response induced by cardiopulmonary bypass. At the cellular level, cardiopulmonary bypass activates leukocytes and

platelets; however the contribution of early (C3a) versus late (C5a, soluble C5b-9) **complement** components to this activation is unclear. We used a model of simulated extracorporeal circulation that activates **complement** (C3a, C5a, and C5b-9 formation), platelets (increased percentages of P-selectin-positive platelets and leukocyte-platelet conjugates), and neutrophils (upregulated CD11b expression). To specifically target **complement** activation in this model, we added a blocking mAb directed at the human C5 **complement** component and assessed its effect on **complement** and cellular activation. Compared with a control mAb, the anti-human C5 mAb profoundly inhibited C5a and soluble C5b-9 generation and serum **complement** hemolytic activity but had no effect on C3a generation. Additionally, the anti-human C5 mAb significantly inhibited neutrophil CD11b upregulation and abolished the increase in P-selectin-positive platelets and leukocyte-platelet conjugate formation compared to experiments performed with the control mAb. This suggests that the terminal components C5a and C5b-9, but not C3a, directly contribute to platelet and neutrophil activation during extracorporeal circulation. Furthermore, these data identify the C5 component as a site for therapeutic intervention in cardiopulmonary bypass.

L14 ANSWER 12 OF 14 BIOSIS COPYRIGHT 1997 BIOSIS
 AN 95:458966 BIOSIS
 DN 98473266
 TI **Complement**-specific antibodies: Designing novel antiinflammatories.
 AU Matis L A; Rollins S A
 CS Immunobiol. Program, Alexion Pharm. Inc., 25 Science Park, Suite 360, New Haven, CT 06511, USA
 SO Nature Medicine 1 (8). 1995. 839-842. ISSN: 1078-8956
 LA English

L14 ANSWER 13 OF 14 BIOSIS COPYRIGHT 1997 BIOSIS
 AN 95:409606 BIOSIS
 DN 98423906
 TI Rapid expression of an anti-human C5 chimeric Fab utilizing a vector that replicates in COS and 293 cells.
 AU Evans M J; Hartman S L; Wolff D W; Rollins S A; Squinto S P
 CS Dep. Mol. Dev., Alexion Pharm. Inc., 25 Science Park, New Haven, CT 06511, USA
 SO Journal of Immunological Methods 184 (1). 1995. 123-138. ISSN: 0022-1759
 LA English
 AB Inhibition of **complement** system activation requires the development of soluble nonimmunogenic inhibitors with good tissue penetrating abilities that are themselves unable to activate **complement**. Chimeric mouse/human Fabs capable of blocking the activity of **complement** proteins are likely to fulfill these criteria. Several monoclonal antibodies that inhibit the activation of the human **complement** system have recently been developed. To examine the properties of chimeric Fab derived from these monoclonal antibodies, we have developed an expression system which allows the rapid production of milligram quantities of chimeric Fab. Both the chimeric light chain and the chimeric Fd were co-expressed from the same vector, pAPEX-3P. This vector contains the SV40 origin of replication, which allows the rapid production of

chimeric Fab in COS cells for preliminary characterization. Additionally, pAPEX-3P contains the Epstein-Barr virus origin of replication and a puromycin selectable marker for maintenance as a stable episome in human cell lines. A production system consisting of transfected 293-EBNA cells cultured in serum free medium followed by protein G-Sepharose chromatography of the conditioned medium was found to be sufficient for the rapid production of purified chimeric Fab. Here we have utilized this expression system to demonstrate that an anti-human C5 chimeric Fab was a potent inhibitor of **complement** activation in both in vitro activation assays and an ex vivo model of **complement**-mediated tissue damage.

L14 ANSWER 14 OF 14 BIOSIS COPYRIGHT 1997 BIOSIS
AN 95:288324 BIOSIS
DN 98302624
TI Monoclonal antibodies to **complement** component C5
in the therapy of inflammatory joint disease.
AU Wang Y; Rollins S R; Madri J A; Elliott E A; Matis L
A
CS Alexion Pharm., New Haven, CT, USA
SO Clinical Research Meeting, San Diego, California, USA, May 5-8, 1995.
Journal of Investigative Medicine 43 (SUPPL. 2). 1995. 362A.
DT Conference
LA English

=> fil hcapolus
'HCAPOLUS' IS NOT A VALID FILE NAME
SESSION CONTINUES IN FILE 'HCAPLUS'

=> fil hcaplus
FILE 'HCAPLUS' ENTERED AT 10:22:53 ON 29 JUL 1997
USE IS SUBJECT TO THE TERMS OF YOUR STN CUSTOMER AGREEMENT.
PLEASE SEE "HELP USAGETERMS" FOR DETAILS.
COPYRIGHT (C) 1997 AMERICAN CHEMICAL SOCIETY (ACS)

Copyright of the articles to which records in this database refer is held by the publishers listed in the PUBLISHER (PB) field (available for records published or updated in Chemical Abstracts after December 26, 1996), unless otherwise indicated in the original publications.

FILE COVERS 1967 - 29 Jul 1997 VOL 127 ISS 5
FILE LAST UPDATED: 29 Jul 1997 (970729/ED)

This file contains CAS Registry Numbers for easy and accurate substance identification.
'OBI' IS DEFAULT SEARCH FIELD FOR 'HCAPLUS' FILE

=> d que 19;d his l10-
L1 (176)SEA FILE=HCAPLUS ABB=ON "EVANS M"/AU OR ("EVANS M J"/AU
OR "EVANS M J B"/AU)
L2 (51)SEA FILE=HCAPLUS ABB=ON "EVANS MARK"/AU OR ("EVANS MARK
J"/AU OR "EVANS MARK JAMES"/AU)
L3 (90)SEA FILE=HCAPLUS ABB=ON ("MATIS L"/AU OR "MATIS L A"/AU
OR "MATIS LOU"/AU OR "MATIS LOUIS"/AU OR "MATIS LOUIS A"/
AU)
L4 (439)SEA FILE=HCAPLUS ABB=ON "MUELLER E"/AU OR "MUELLER E E"/
AU
L5 (4)SEA FILE=HCAPLUS ABB=ON "MUELLER EILEEN ELLIOTT"/AU
L6 (21)SEA FILE=HCAPLUS ABB=ON "NYE S"/AU OR ("NYE STEVEN"/AU O
R "NYE STEVEN H"/AU OR "NYE STEVEN HOWARD"/AU)
L7 (766)SEA FILE=HCAPLUS ABB=ON L1 OR L2 OR L3 OR L4 OR L5 OR L6

L8 (46)SEA FILE=HCAPLUS ABB=ON ("ROLLINS S N"/AU OR "ROLLINS S
R"/AU) OR ("ROLLINS SCOTT"/AU OR "ROLLINS SCOTT A"/AU OR
"ROLLINS SCOTT ALAN"/AU)
L9 795 SEA FILE=HCAPLUS ABB=ON L8 OR L7

(FILE 'HCAPLUS' ENTERED AT 10:20:41 ON 29 JUL 1997)

L10 469 S COMPLEMENT AND C5
L11 12 S L10 AND L9
L12 5933 S ALPHA (2W) CHAIN# OR (ALPAH (2W) CHAIN#)/AB
L13 13740 S L12 OR (ALPHA (2W) CHAIN#)/AB
L14 33 S L13 AND L10
L15 3 S L14 AND (ANTI OR ANTIBOD?)
L16 12 S L11 NOT L15

FILE 'HCAPLUS' ENTERED AT 10:22:53 ON 29 JUL 1997

=> d .ca l15 1-3;d .ca 1-12

L15 ANSWER 1 OF 3 HCAPLUS COPYRIGHT 1997 ACS

AN 1993:122866 HCAPLUS
 DN 118:122866
 TI Molecular basis of **complement** resistance of human melanoma cells expressing the C3-cleaving membrane protease p65
 AU Ollert, Markus W.; Kadlec, Joseph V.; Petrella, Eugene C.; Bredehorst, Reinhard; Vogel, Carl Wilhelm
 CS Sch. Med., Georgetown Univ., Washington, DC, 20007, USA
 SO Cancer Res. (1993), 53(3), 592-9
 CODEN: CNREA8; ISSN: 0008-5472
 DT Journal
 LA English
 AB The mol. mechanism of complement resistance of the human SK-MEL-170 melanoma cell line was investigated. The cells have been shown to express the C3b-cleaving membrane protease p65. To delineate the mol. consequences of the C3b-cleaving activity for the complement cytotoxicity, the mol. events during the initiation (R24 monoclonal antibody, C1), amplification (C4, C3), and membrane attack (C5, C9) phases of complement were studied in comparison to a complement-susceptible human melanoma line (SK-MEL-93-2). No cleavage of C4b and C5b, 2 mols. structurally similar to C3b, was obsd. on the cells during classical pathway activation indicating the specificity of the p65 protease for the C3b mol. The rapid degrdn. of C3b by p65 on the surface of complement-resistant SK-MEL-170 cells generates a mol. wt. 30,000 C3.**alpha**.'-**chain**-fragment detectable as early as 1 min after complement activation, whereas no such fragment was present in detectable amts. on complement-susceptible cells. As a result of the rapid C3b proteolysis by p65 on resistant SK-MEL-170 cells, less C5 convertases are formed, which in turn results in the formation of a lower no. of terminal complement components and membrane attack complexes. R24 antibody and C1q binding to the resistant cells was slightly lower as to susceptible cells. C4 binding studies, however, revealed that the obsd. difference in antibody and C1q binding has no influence on the complement resistance of SK-MEL-170 cells: more C4b was bound to complement-resistant (1565 fg/cell) as compared to susceptible cells (715 fg/cell). On extn. of the mol. forms of C4 bound to the cell membranes, an addnl. high mol. wt. C4 species, apparently a C4b-C4b homodimer, appeared only on the resistant SK-MEL-170 cells that may function as a residual back-up C5 convertase. Thus, collectively, SK-MEL-170 human melanoma cells evade complement-mediated cytolysis despite sufficient activation of early components of the classical complement pathway by p65-mediated rapid degrdn. of surface-bound C3b, leading to a redn. in membrane attack complex formation. Rapid cleavage of surface deposited C3b was thus established as a powerful mechanism of complement resistance.
 CC 15-8 (Immunocytochemistry)
 ST **complement** resistance melanoma C3b protease p65
 IT Melanoma
 (**complement** resistance by human, C3b-cleaving membrane protease p65 in)
 IT Cytolysis
 (**complement**-mediated, human melanoma cell resistance to, membrane protease in)
 IT Cell membrane
 (protease p65 of, of human melanoma cells, in resistance to **complement**)
 IT **Complement**
 RL: BIOL (Biological study)

(classical pathway, melanoma cells resistance to, of humans, membrane protease in)

IT **Antibodies**

RL: BIOL (Biological study)

(monoclonal, to ganglioside GD3 on human melanoma cells, **complement** activation by, melanoma resistance to, membrane protease in)

IT 62010-37-1, Ganglioside GD3

RL: BIOL (Biological study)

(**antibody** to, **complement** activation by, human melanoma cells resistance to, C3b-cleaving membrane protease in)

IT 60831-94-9, **Complement C5** convertase

82986-89-8, **Complement C 5b9**

RL: FORM (Formation, nonpreparative)

(formation of, human melanoma cell inhibition of, C3b-cleaving membrane protease in)

IT 80295-50-7, **Complement C4b**

RL: BIOL (Biological study)

(homodimer of, on human melanoma cells, membrane protease and **complement** resistance in relation to)

IT 80295-41-6, **Complement C3**

RL: BIOL (Biological study)

(melanoma cell binding of human, membrane protease and **complement** resistance in relation to)

IT 80295-43-8, **Complement C3b**

RL: BIOL (Biological study)

(membrane protease p65 of human melanoma cell hydrolysis of, **complement** resistance in relation to)

IT 128689-72-5, **Complement C3b** proteinase

RL: BIOL (Biological study)

(of melanoma cells of humans, in **complement** resistance)

L15 ANSWER 2 OF 3 HCAPLUS COPYRIGHT 1997 ACS

AN 1988:547624 HCAPLUS

DN 109:147624

TI Use of antisera to the isolated alpha and beta subunits of C3 as probes to study functional sites present on particle-bound C3b but absent on native soluble forms of C3

AU Whaley, K.; Nilsson, Ulf

CS West. Infirm., Univ. Glasgow, Glasgow, UK

SO Int. Arch. Allergy Appl. Immunol. (1988), 86(1), 55-61

CODEN: IAAAAM; ISSN: 0020-5915

DT Journal

LA English

AB The effect of antisera to the isolated .alpha. and .beta. chains of complement C3 on certain C3b-dependent reactions has been studied. C5-mediated hemolysis of erythrocyte-antibody-C1423b was inhibited preferentially by antiserum to the .alpha. chain, whereas antiserum to the .beta. chain inhibited the formation of C3bBb. The anti-.beta. chain antiserum also stabilized C3bBbP, and rendered the enzyme relatively resistant to accelerated decay in the presence of factor H. These and previous findings that anti-.alpha. and anti-.beta. IgG bind to restricted subsets of antigenic determinants on C3/C3b suggest that these antisera affect C3b function through the binding of antibodies to active binding sites exclusively exposed by bound C3b.

CC 15-4 (Immunochemistry)

ST **complement C3 alpha beta subunit antibody**

IT Hemolysis

- (**complement** C3-mediated, **antibodies** to C3 subunits effect on, of humans)
- IT **Antibodies**
 RL: BIOL (Biological study)
 (to **complement** C3 subunits, **complement** C3-mediated activities response to, of humans)
- IT 80295-43-8, **Complement** C3b
 RL: BIOL (Biological study)
 (**antibodies** to C3 subunits effect on activities of, of humans)
- IT 80295-65-4
 RL: BIOL (Biological study)
 (**complement** convertase resistance to, **antibodies** to **complement** C3 subunits effect on, of humans)
- IT 80295-53-0, **Complement** C5
 RL: BIOL (Biological study)
 (hemolysis mediated by, **antibodies** to **complement** C3 subunits effect on, of humans)
- IT 77000-02-3
 RL: PROC (Process)
 (stabilization of, by **antibodies** to C3 subunits, of humans)
- IT 80295-41-6, **Complement** C3
 RL: BIOL (Biological study)
 (.alpha.- and .beta.-subunits of, **antibodies** to, C3-mediated activities response to, of humans)
- L15 ANSWER 3 OF 3 HCAPLUS COPYRIGHT 1997 ACS
 AN 1986:146822 HCAPLUS
 DN 104:146822
 TI Parameters of the stimulation of human monocytes by factor B of the **complement** system
 AU Baumgarten, H.; Opperman, M.; Schulze, M.; Goetze, O.
 CS Zent. Hyg. Humangenet., Universitaetsklin. Goettingen, Goettingen, D-3400, Fed. Rep. Ger.
 SO Mononucle. Phagocytes, [Proc. Conf.], 4th (1985), Meeting Date 1984, 163-71. Editor(s): Van Furth, Ralph. Publisher: Nijhoff, Dordrecht, Neth.
 CODEN: 54WAAX
 DT Conference
 LA English
 AB Evidence is provided for a complement factor B (Bb)-dependent stimulation of human monocytes with respect to the secretion of lysosomal hydrolases and H2O2 and to receptor-mediated phagocytosis. It is further demonstrated that divalent antibody mols. specific for the C5a region of the .alpha.-chain of C5 are able to induce the secretion of lysosomal hydrolases in the absence of any other added stimulus. Probably membrane-assocd. (m)C5 is oriented in the monocyte plasma membrane in such a way that the C5a portion of its .alpha.-chain is accessible to antibody added to the outside of the cell. Apparently, the cleavage site for Bb on the .alpha.-chain of mC5 is externally disposed, so the obsd. effects of Bb on human monocytes are caused by the generation of mC5 and C5a.
 CC 15-4 (Immunocytochemistry)
 ST monocyte stimulation **complement** factor Bb
 IT Phagocytosis
 (by macrophage, **complement** factor Bb stimulation of, of

human)
 IT Monocyte
 (hydrogen peroxide and hydrolase release from and phagocytosis
 by, **complement** factor Bb stimulation of, of human)
 IT Lysosome
 (hydrolases of, **complement** factor Bb-stimulated release
 of, from human macrophage)
 IT **Antibodies**
 RL: BIOL (Biological study)
 (to **complement** C5a, lysosomal hydrolase release from
 human monocyte induction by, **complement** factor Bb in
 relation to)
 IT 80295-54-1
 RL: FORM (Formation, nonpreparative)
 (formation of, factor Bb stimulation of human monocyte response
 to, membrane-assocd. **C5** in relation to)
 IT 82532-87-4
 RL: BIOL (Biological study)
 (hydrogen peroxide and hydrolase release and phagocytosis by
 macrophage induction by, **complement** **C5** in
 relation to, of human)
 IT 7722-84-1, biological studies 9001-77-8 9012-33-3
 RL: BIOL (Biological study)
 (release of, from monocyte of human, **complement** factor
 Bb stimulation of)

L16 ANSWER 1 OF 12 HCAPLUS COPYRIGHT 1997 ACS
 AN 1997:430905 HCAPLUS
 TI Amelioration of lupuslike autoimmune disease in NZB/W F1 mice after
 treatment with a blocking monoclonal antibody specific for
 complement component **C5**
 AU Wang, Yi; Hu, Qile; Madri, Joseph A.; Rollins, Scott A.;
 Chodera, Amy; Matis, Louis A.
 CS Alexion Pharmaceuticals, 25 Science Park, New Haven, CT, 06511, USA
 SO Controlling Complement Syst. Novel Drug Dev., [IBC Conf.] (1997),
 89-109. Editor(s): Mazarakis, Helen; Swart, Sarah Jane. Publisher:
 International Business Communications, Southborough, Mass.
 CODEN: 64QOAM
 DT Conference
 LA English
 AB New Zealand black .times. New Zealand white (NZB/W) F1 mice
 spontaneously develop an autoimmune syndrome with notable
 similarities to human systemic lupus erythematosus (SLE). Female
 NZB/W F1 mice produce high titers of antinuclear antibodies and
 invariably succumb to severe glomerulonephritis by 12 mo of age.
 Although the development of the immune-complex nephritis is
 accompanied by abundant local and systemic complement activation,
 the role of pro-inflammatory complement components in disease
 progression has not been established. In this study we have examd.
 the contribution of activated terminal complement proteins to the
 pathogenesis of the lupuslike autoimmune disease. Female NZB/W F1
 mice were treated with a monoclonal antibody (mAb) specific for the
 C5 component of complement that blocks the coverage of C5 and thus
 prevents the generation of the potent pro-inflammatory factors C5a
 and C5b-9. Continuous therapy with anti-C5 mAb for six months
 resulted in significant amelioration of the course of
 CC 15 (Immunochemistry)

L16 ANSWER 2 OF 12 HCAPLUS COPYRIGHT 1997 ACS

AN 1997:348505 HCAPLUS

TI Inhibition of **complement** activity by humanized anti-C5 antibody and single-chain Fv

AU Thomas, Thomas C.; **Rollins, Scott A.**; Rother, Russell P.; Giannoni, Michelle A.; Hartman, Sandra L.; Elliott, Eileen A.; **Nye, Steven H.**; **Matis, Louis A.**; Squinto, Stephen P.; **Evans, Mark J.**

CS Alexion Pharmaceuticals, New Haven, CT, 06511, USA

SO Mol. Immunol. (1997), 33(17/18), 1389-1401

CODEN: MOIMD5; ISSN: 0161-5890

PB Elsevier

DT Journal

LA English

AB Activation of the complement system contributes significantly to the pathogenesis of numerous acute and chronic diseases. Recently, a monoclonal antibody (5G1.1) that recognizes the human complement protein C5, has been shown to effectively block C5 cleavage, thereby preventing the generation of the pro-inflammatory complement components C5a and C5b-9. Humanized 5G1.1 antibody, Fab and scFv mols. have been produced by grafting the complementarity detg. regions of 5G1.1 on to human framework regions. Competitive ELISA anal. indicated that no framework changes were required in the humanized variable regions for retention of high affinity binding to C5, even at framework positions predicted by computer modeling to influence CDR canonical structure. The humanized Fab and scFv mols. blocked complement-mediated lysis of chicken erythrocytes and porcine aortic endothelial cells in a dose-dependent fashion, with complete complement inhibition occurring at a three-fold molar excess, relative to the human c5 concn. In contrast to a previously characterized anti-C5 scFv mol., the humanized h5G1.1 scFv also effectively blocked C5a generation. Finally, an intact humanized h5G1.1 antibody blocked human complement lytic activity at concns. identical to the original murine monoclonal antibody. These results demonstrate that humanized h5G1.1 and its recombinant derivs. retain both the affinity and blocking functions of the murine 5G1.1 antibody, and suggest that these mols. may serve as potent inhibitors of complement-mediated pathol. in human inflammatory diseases.

CC 15 (Immunochemistry)

L16 ANSWER 3 OF 12 HCAPLUS COPYRIGHT 1997 ACS

AN 1996:498766 HCAPLUS

DN 125:165528

TI Amelioration of lupus-like autoimmune disease in NZB/W F1 mice after treatment with a blocking monoclonal antibody specific for **complement** component C5

AU Wang, Yi; Hu, Qile; Madri, Joseph A.; **Rollins, Scott A.**; Chodera, Amy; **Matis, Louis A.**

CS Immunobiology Program, Alexion Pharmaceuticals, Inc., New Haven, CT, 06511, USA

SO Proc. Natl. Acad. Sci. U. S. A. (1996), 93(16), 8563-8568

CODEN: PNASA6; ISSN: 0027-8424

DT Journal

LA English

AB New Zealand black .times. New Zealand white (NZB/W) F1 mice spontaneously develop an autoimmune syndrome with notable similarities to human systemic lupus erythematosus. Female NZB/W F1

mice produce high titers of antinuclear antibodies and invariably succumb to severe glomerulonephritis by 12 mo of age. Although the development of the immune-complex nephritis is accompanied by abundant local and systemic complement activation, the role of proinflammatory complement components in disease progression has not been established. Here, the authors examd. the contribution of activated terminal complement proteins to the pathogenesis of the lupus-like autoimmune disease. Female NZB/W F1 mice were treated with a monoclonal antibody (mAb) specific for the C5 component of complement that blocks the cleavage of C5 and thus prevents the generation of the potent proinflammatory factors C5a and C5b-9. Continuous therapy with anti-C5 mAb for 6 mo resulted in amelioration of the course of glomerulonephritis and in markedly increased survival. These findings demonstrate an important role for the terminal complement cascade in the progression of renal disease in NZB/W F1 mice, and suggest that mAb-mediated C5 inhibition may be a useful approach to the therapy of immune-complex glomerulonephritis in humans.

CC 15-8 (Immunochemistry)
 ST lupus model monoclonal antibody **complement C5**
 IT Lupus erythematosus
 (terminal **complement** cascade role in lupus
 erythematosus model)
 IT Kidney, disease
 (immune complex glomerulonephritis, terminal **complement**
 cascade role in lupus erythematosus model)
 IT Antibodies
 RL: BAC (Biological activity or effector, except adverse); THU
 (Therapeutic use); BIOL (Biological study); USES (Uses)
 (monoclonal, amelioration of lupus-like autoimmune disease in
 mice after treatment with blocking monoclonal antibody to
 complement component C5)
 IT 80295-53-0, **Complement C5**
 RL: BSU (Biological study, unclassified); BIOL (Biological study)
 (amelioration of lupus-like autoimmune disease in mice after
 treatment with blocking monoclonal antibody to **complement**
 component C5)
 IT 82986-89-8, **Complement C5b-9**
 RL: ADV (Adverse effect, including toxicity); BIOL (Biological
 study)
 (terminal **complement** cascade role in lupus
 erythematosus model)

L16 ANSWER 4 OF 12 HCAPLUS COPYRIGHT 1997 ACS
 AN 1996:365806 HCAPLUS
 DN 125:26270
 TI Methods for the treatment of inflammatory joint disease with
 compounds that block **complement** component C5
 IN Wang, Yi; Matis, Louis
 PA Alexion Pharmaceuticals, Inc., USA
 SO PCT Int. Appl., 69 pp.
 CODEN: PIXXD2
 PI WO 9609043 A1 960328
 DS W: AU, CA, JP
 RW: AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE
 AI WO 95-US12404 950921
 PRAI US 94-311489 940923
 DT Patent
 LA English

AB The use of compds. that block complement component C5 or its active fragments C5a and/or C5b (collectively referred to as "C5 blockers") to treat established joint inflammation (arthritis) is disclosed. Administration of such C5 blockers has been found to (1) arrest and/or reduce inflammation in joints which are already inflamed and (2) inhibit the spread of inflammation to unaffected joints. The C5 blockers include e.g. proteins (including antibodies) and peptides. Results using a monoclonal antibody C5 blocker are presented.

IC ICM A61K031-395
ICS A61K031-34; C07D307-94; C07K016-18; C07K016-40

CC 1-7 (Pharmacology)
Section cross-reference(s): 15

ST **complement C5** blocker antiinflammatory arthritis; monoclonal antibody **complement C5** antiarthritic

IT Cytolysis
(by **complement**; **complement C5** blockers for treatment of inflammatory joint disease)

IT Inflammation inhibitors
(**complement C5** blockers for treatment of inflammatory joint disease)

IT Blood serum
Blood
(**complement C5** blockers for treatment of inflammatory joint disease in relation to redn. of cell-lysing ability of **complement** in blood-derived fluid)

IT Synovial fluid
(**complement C5** blockers for treatment of inflammatory joint disease in relation to redn. of cell-lysing ability of **complement** in synovial fluid)

IT **Complement**
RL: BPR (Biological process); BIOL (Biological study); PROC (Process)
(cytolysis by; **complement C5** blockers for treatment of inflammatory joint disease)

IT Inflammation inhibitors
(antiarthritics, **complement C5** blockers for treatment of inflammatory joint disease)

IT Joint, anatomical
(disease, inflammation, **complement C5** blockers for treatment of inflammatory joint disease)

IT Antibodies
RL: BAC (Biological activity or effector, except adverse); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(monoclonal, anti-C5; **complement C5** blockers for treatment of inflammatory joint disease)

IT 80295-53-0, **Complement C5** 80295-54-1, **Complement C5a** 80295-55-2, **Complement C5b** 82986-89-8, **Complement C5b9**
RL: BPR (Biological process); BIOL (Biological study); PROC (Process)
(**complement C5** blockers for treatment of inflammatory joint disease)

L16 ANSWER 5 OF 12 HCAPLUS COPYRIGHT 1997 ACS
AN 1996:298330 HCAPLUS
DN 124:325364
TI Retroviral transduction of cells using soluble **complement** inhibitors

IN Rother, Russell P.; **Rollins, Scott A.**; Mason, James M.;
Squinto, Stephen P.
PA Alexion Pharmaceuticals, Inc., USA
SO PCT Int. Appl., 49 pp.
CODEN: PIXXD2
PI WO 9603146 A1 960208
DS W: AU, CA, JP
RW: AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE
AI WO 95-US8924 950714
PRAI US 94-278550 940721
DT Patent
LA English
AB Methods and compns. are provided for facilitating gene therapy
procedures involving the transduction of target cells with
retroviral vector particles in the presence of complement-contg.
body fluids. The administration of sol. complement inhibitor mols.
to body fluids prevents the complement-mediated inactivation of the
retroviral vector particles, and provides a safety mechanism for
such gene therapy procedures, as the action of sol. complement
inhibitors is transient, and any retroviral vector particles present
after the return of uninhibited complement activity will be
inactivated.
IC ICM A61K039-395
CC 63-3 (Pharmaceuticals)
Section cross-reference(s): 1
ST retrovirus transduction **complement** inhibitor gene therapy
IT **Complement**
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(inhibitors; retroviral transduction of cells using sol.
complement inhibitors)
IT Blood plasma
Blood serum
Blood
Signal transduction, biological
(retroviral transduction of cells using sol. **complement**
inhibitors)
IT Therapeutics
(geno-, retroviral transduction of cells using sol.
complement inhibitors)
IT Antibodies
RL: THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(monoclonal, anti-**complement**; retroviral transduction
of cells using sol. **complement** inhibitors)
IT Virus, animal
(retro-, retroviral transduction of cells using sol.
complement inhibitors)
IT 80295-53-0, **Complement C5**
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(inhibitors; retroviral transduction of cells using sol.
complement inhibitors)
L16 ANSWER 6 OF 12 HCAPLUS COPYRIGHT 1997 ACS
AN 1996:73261 HCAPLUS
DN 124:127101
TI Anti-**complement C5** antibodies for the treatment
of glomerulonephritis and other inflammatory diseases
IN **Evans, Mark J.**; **Matis, Louis**; **Mueller,**
Eileen Elliott; **Nye, Steven H.**; **Rollins,**
Scott; Rother, Russell P.; Springhorn, Jeremy P.; Squinto,

Stephen P.; Thomas, Thomas C.; et al.
 PA Alexion Pharmaceuticals, Inc., USA
 SO PCT Int. Appl., 159 pp.
 CODEN: PIXXD2
 PI WO 9529697 A1 951109
 DS W: AM, AU, BB, BG, BR, BY, CA, CN, CZ, EE, FI, GE, HU, IS, JP, KG,
 KP, KR, KZ, LK, LR, LT, LV, MD, MG, MN, MX, NO, NZ, PL, RO, RU,
 SG, SI, SK, TJ, TM, TT, UA, UG, US, UZ, VN
 RW: AT, BE, BF, BJ, CF, CG, CH, CI, CM, DE, DK, ES, FR, GA, GB, GR,
 IE, IT, LU, MC, ML, MR, NE, NL, PT, SE, SN, TD, TG
 AI WO 95-US5688 950501
 PRAI US 94-236208 940502
 DT Patent
 LA English
 AB The use of anti-C5 antibodies, e.g., monoclonal antibodies, to treat
 glomerulonephritis (GN) is disclosed. The administration of such
 antibodies at low dosage levels has been found to significantly
 reduce glomerular inflammation/enlargement and other pathol.
 conditions assocd. with GN. Also disclosed are novel anti-C5
 antibodies and anti-C5 antibody-encoding nucleic acid mols. These
 antibodies are useful in the treatment of GN and other inflammatory
 conditions involving pathol. activation of the complement system.
 IC ICM A61K038-36
 ICS A61K039-00; A61K039-395; C07K014-00; C07K014-75; C07K016-00;
 C07K016-18; C07K016-36; C07K016-46; C12N005-10; C12N005-20;
 C12N015-09; C12N015-10; C12N015-13; C12N015-63; C12P021-02;
 C12P021-08
 CC 63-3 (Pharmaceuticals)
 Section cross-reference(s): 3, 15
 ST antibody **complement C5** cloning
 glomerulonephritis sequence
 IT Antigens
 RL: BSU (Biological study, unclassified); BIOL (Biological study)
 (KSSKC epitope, antibodies binding to; anti-**complement**
C5 antibodies for the treatment of glomerulonephritis and
 other inflammatory diseases)
 IT Hybridoma
 Molecular cloning
 Packaging materials
 Polymerase chain reaction
 Protein sequences
 (anti-**complement C5** antibodies for the
 treatment of glomerulonephritis and other inflammatory diseases)
 IT Immune complexes
 RL: BPR (Biological process); BIOL (Biological study); PROC
 (Process)
 (deposition of; anti-**complement C5** antibodies
 for the treatment of glomerulonephritis and other inflammatory
 diseases)
 IT Immunoglobulins
 RL: BAC (Biological activity or effector, except adverse); BPN
 (Biosynthetic preparation); PRP (Properties); THU (Therapeutic use);
 BIOL (Biological study); PREP (Preparation); USES (Uses)
 (G, anti-**complement C5** antibodies for the
 treatment of glomerulonephritis and other inflammatory diseases)
 IT Deoxyribonucleic acid sequences
 (complementary, anti-**complement C5** antibodies
 for the treatment of glomerulonephritis and other inflammatory
 diseases)

- IT Kidney, disease
(glomerulonephritis, anti-**complement C5**
antibodies for the treatment of glomerulonephritis and other
inflammatory diseases)
- IT Proteins, biological studies
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(metabolic disorders, proteinuria, inhibition of; anti-
complement C5 antibodies for the treatment of
glomerulonephritis and other inflammatory diseases)
- IT Antibodies
RL: BAC (Biological activity or effector, except adverse); BPN
(Biosynthetic preparation); PRP (Properties); THU (Therapeutic use);
BIOL (Biological study); PREP (Preparation); USES (Uses)
(monoclonal, anti-**complement C5** antibodies
for the treatment of glomerulonephritis and other inflammatory
diseases)
- IT 173016-57-4
RL: NUU (Nonbiological use, unclassified); PRP (Properties); USES
(Uses)
(PCR primer UDEC395; anti-**complement C5**
antibodies for the treatment of glomerulonephritis and other
inflammatory diseases)
- IT 173016-56-3
RL: NUU (Nonbiological use, unclassified); PRP (Properties); USES
(Uses)
(PCR primer UDEC690; anti-**complement C5**
antibodies for the treatment of glomerulonephritis and other
inflammatory diseases)
- IT 172893-24-2P 173011-96-6P 173012-10-7P 173012-12-9P 173012-1
4-1P 173012-17-4P 173012-19-6P 173012-21-0P 173012-23-2P
173012-25-4P 173012-27-6P 173012-29-8P
RL: BAC (Biological activity or effector, except adverse); BOC
(Biological occurrence); BPN (Biosynthetic preparation); PRP
(Properties); THU (Therapeutic use); BIOL (Biological study); OCCU
(Occurrence); PREP (Preparation); USES (Uses)
(amino acid sequence; anti-**complement C5**
antibodies for the treatment of glomerulonephritis and other
inflammatory diseases)
- IT 173012-07-2, **Complement C5**, prepro- (human)
RL: BOC (Biological occurrence); PRP (Properties); THU (Therapeutic
use); BIOL (Biological study); OCCU (Occurrence); USES (Uses)
(amino acid sequence; anti-**complement C5**
antibodies for the treatment of glomerulonephritis and other
inflammatory diseases)
- IT 80295-53-0, **Complement c5**
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(antibodies to; anti-**complement C5** antibodies
for the treatment of glomerulonephritis and other inflammatory
diseases)
- IT 172998-82-2P
RL: BPN (Biosynthetic preparation); PRP (Properties); THU
(Therapeutic use); BIOL (Biological study); PREP (Preparation); USES
(Uses)
(epitope KSSKC-contg. antigen; anti-**complement**
C5 antibodies for the treatment of glomerulonephritis and
other inflammatory diseases)
- IT 173012-09-4P 173012-11-8P 173012-13-0P 173012-15-2P
173012-16-3P 173012-18-5P 173012-20-9P 173012-22-1P
173012-24-3P 173012-26-5P 173012-28-7P 173012-30-1P

RL: BAC (Biological activity or effector, except adverse); BOC (Biological occurrence); BPN (Biosynthetic preparation); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); OCCU (Occurrence); PREP (Preparation); USES (Uses)

(nucleic acid sequence; anti-**complement C5** antibodies for the treatment of glomerulonephritis and other inflammatory diseases)

IT 173146-43-5, Deoxyribonucleic acid (plasmid Apex-1) 173146-44-6, Deoxyribonucleic acid (plasmid Apex-3P) 173146-45-7

RL: BUU (Biological use, unclassified); PRP (Properties); BIOL (Biological study); USES (Uses)

(nucleic acid sequence; anti-**complement C5** antibodies for the treatment of glomerulonephritis and other inflammatory diseases)

L16 ANSWER 7 OF 12 HCAPLUS COPYRIGHT 1997 ACS

AN 1996:54415 HCAPLUS

DN 124:114995

TI In vitro and in vivo inhibition of **complement** activity by a single-chain Fv fragment recognizing human **C5**

AU **Evans, Mark J.; Rollins, Scott A.; Wolff, Dennis W.; Rother, Russell P.; Norin, Allen J.; Therrien, Denise M.; Grijalva, Galo A.; Mueller, John P.; Nye, Steven H.; et al.**

CS Dep. of Mol. Development, Alexion Pharmaceuticals, New Haven, CT, 06511, USA

SO Mol. Immunol. (1995), 32(16), 1183-95

CODEN: MOIMD5; ISSN: 0161-5890

DT Journal

LA English

AB Complement activation has been implicated in the pathogenesis of several human diseases. Recently, a monoclonal antibody (N19-8) that recognizes the human complement protein C5 has been shown to effectively block the cleavage of C5 into C5a and C5b, thereby blocking terminal complement activation. In this study, a recombinant N19-8 scFv antibody fragment was constructed from the N19-8 variable regions, and produced in both mammalian and bacterial cells. The N19-8 scFv bound human C5 and was as potent as the N19-8 monoclonal antibody at inhibiting human C5b-9-mediated hemolysis of chicken erythrocytes. In contrast, the N19-8 scFv only partially retained the ability of the N19-8 monoclonal antibody to inhibit C5a generation. To investigate the ability of the N19-8 scFv to inhibit complement-mediated tissue damage, complement-dependent myocardial injury was induced in isolated mouse hearts by perfusion with Krebs-Henseleit buffer contg. 6% human plasma. The perfused hearts sustained extensive deposition of human C3 and C5b-9, resulting in increased coronary artery perfusion pressure, end-diastolic pressure, and a decrease in heart rate until the hearts ceased beating approx. 10 min after the addn. of plasma. Hearts treated with human plasma supplemented with either the N19-8 monoclonal antibody or the N19-8 monoclonal antibody or the N19-8 scFv did not show any detectable changes in cardiac performance for at least 1 h following the addn. of plasma. Hearts treated with human plasma alone showed extensive deposition of C3 and C5b-9, while hearts treated with human plasma contg. the N19-8 scFv showed extensive deposition of C3, but no detectable deposition of C5b-9. Administration of a 100 mg bolus dose of N19-8 scFv to rhesus monkeys inhibited the serum hemolytic activity by at least 50% for up to 2 h. Pharmacokinetic anal. of N19-8 scFv serum levels

suggested a two-compartment model with a $T_{1/2}$ of 27 min. These data suggest that recombinant N19-8 scFv is a potent inhibitor of the terminal complement cascade and may have potential in vivo applications where short duration inhibition of terminal complement activity is desirable.

- CC 15-4 (Immunochemistry)
- ST **complement C5** inhibition Ig Fv fragment; single chain Ig **complement C5** inhibition
- IT Deoxyribonucleic acid sequences
 Mouse
 Protein sequences
 (**complement** activity inhibition by a single-chain Fv fragment recognizing human **C5**)
- IT **Complement**
 RL: ADV (Adverse effect, including toxicity); BIOL (Biological study)
 (**complement** activity inhibition by single-chain Fv fragment recognizing human **C5**)
- IT Immunoglobulins
 RL: BAC (Biological activity or effector, except adverse); BIOL (Biological study)
 (single-chain Fv fragment; **complement** activity inhibition by single-chain Fv fragment recognizing human **C5**)
- IT 172893-24-2
 RL: PRP (Properties)
 (amino acid sequence; **complement** activity inhibition by a single-chain Fv fragment recognizing human **C5**)
- IT 80295-53-0, **Complement c5**
 RL: ADV (Adverse effect, including toxicity); BIOL (Biological study)
 (**complement** activity inhibition by single-chain Fv fragment recognizing human **C5**)
- IT 82986-89-8, **Complement c5b-9**
 RL: BPR (Biological process); BIOL (Biological study); PROC (Process)
 (hemolysis; **complement** activity inhibition by a single-chain Fv fragment recognizing human **C5**)
- IT 166845-08-5, Genbank L43067
 RL: PRP (Properties)
 (nucleotide sequence; **complement** activity inhibition by a single-chain Fv fragment recognizing human **C5**)
- L16 ANSWER 8 OF 12 HCAPLUS COPYRIGHT 1997 ACS
- AN 1996:49519 HCAPLUS
- DN 124:143157
- TI Monoclonal antibodies directed against human **C5** and **C8** block **complement**-mediated damage of xenogeneic cells and organs
- AU Rollins, Scott A.; Matis, Louis A.; Springhorn, Jeremy P.; Setter, Eva; Wolff, Dennis W.
- CS Department of Immunobiology, Alexion Pharmaceuticals, Inc., New haven, CT, 06511, USA
- SO Transplantation (1995), 60(11), 1284-92
 CODEN: TRPLAU; ISSN: 0041-1337
- DT Journal
- LA English
- AB The hyperacute rejection (HAR) of xenotransplanted organs is initiated by the deposition of natural antibodies on donor

endothelium followed by the activation of the recipient complement system, which rapidly destroys the graft. Studies of the role of activated complement in HAR have suggested that natural antibody as well as early (C3a, C3b) and the late (C5a, C5b-9) activated complement components may contribute to cell activation and damage. Attenuation of HAR has been achieved by blockade of C3 activation with sol. CR1 or consumptive depletion of complement with cobra venom factor; however, similar studies using specific inhibitors of terminal complement components have not been described. To address the contribution of C5a and the membrane attack complex (C5b-9, MAC) to complement-mediated xenogeneic cell and organ damage, we utilized functionally blocking monoclonal antibodies directed against the human terminal complements components C5 and C8. Our data show that both anti-C5 and anti-C8 mAbs protect porcine aortic endothelial cells from membrane damage mediated by human C5b-9. Addnl., both the anti-C5 and anti-C8 mAbs blocked complement-mediated generation of membrane prothrombinase activity on porcine aortic endothelial cells challenged with human serum. To test the ability of these antibodies to attenuate antibody and complement-mediated damage of xenogeneic organs, an ex vivo model was developed wherein isolated rat hearts were perfused with human serum in the presence or absence of the anti-C5 and anti-C8 mAbs. Our data demonstrate that mAbs directed against human C5 and C8 prevented organ damage by human serum complement and suggest that these mols. may serve as potent inhibitors of HAR.

- CC 15-4 (Immunochemistry)
 ST monoclonal antibody **complement C5 C8**
 IT Cytolysis
 (monoclonal antibodies to human **C5** and **C8** block **complement**-mediated damage of xenogeneic cells and organs)
 IT **Complement**
 RL: ADV (Adverse effect, including toxicity); BIOL (Biological study)
 (monoclonal antibodies to human **C5** and **C8** block **complement**-mediated damage of xenogeneic cells and organs)
 IT Blood vessel, disease
 (endothelium, injury, monoclonal antibodies to human **C5** and **C8** block **complement**-mediated damage of xenogeneic cells and organs)
 IT Heart, disease
 (injury, monoclonal antibodies to human **C5** and **C8** block **complement**-mediated damage of xenogeneic cells and organs)
 IT Antibodies
 RL: BAC (Biological activity or effector, except adverse); BIOL (Biological study)
 (monoclonal, monoclonal antibodies to human **C5** and **C8** block **complement**-mediated damage of xenogeneic cells and organs)
 IT Transplant and Transplantation
 (xeno-, monoclonal antibodies to human **C5** and **C8** block **complement**-mediated damage of xenogeneic cells and organs in relation to)
 IT 80295-53-0, **Complement c5** 80295-58-5, **Complement c8**
 RL: BSU (Biological study, unclassified); BIOL (Biological study)
 (monoclonal antibodies to human **C5** and **C8** block

complement-mediated damage of xenogeneic cells and organs)

IT 80295-54-1, **Complement** C5a
 RL: BSU (Biological study, unclassified); BIOL (Biological study)
 (role of C5a in **complement**-mediated damage of xenogeneic cells and organs)

IT 82986-89-8, **Complement** C5b-9
 RL: BSU (Biological study, unclassified); BIOL (Biological study)
 (role of C5b-9 in **complement**-mediated damage of xenogeneic cells and organs)

L16 ANSWER 9 OF 12 HCAPLUS COPYRIGHT 1997 ACS
 AN 1996:49512 HCAPLUS
 DN 124:143156
 TI **Complement** inhibition with an anti-C5 monoclonal antibody prevents acute cardiac tissue injury in an ex vivo model of pig-to-human xenotransplantation

AU Kroshus, Timothy J.; Rollins, Scott A.; Dalmasso, Agustin P.; Elliott, Eileen A.; Matis, Louis A.; Squinto, Stephen P.; Bolman, R. Morton, III
 CS Department of Surgery, University of Minnesota, Minneapolis, MN, USA
 SO Transplantation (1995), 60(11), 1194-202
 CODEN: TRPLAU; ISSN: 0041-1337
 DT Journal
 LA English
 AB Prevention of hyperacute xenograft rejection in the pig-to-primate combination has been accomplished by removal of natural antibodies, complement depletion with cobra venom factor, or prevention of C3 activation with the sol. complement inhibitor SCR1. Although these strategies effectively prevent hyperacute rejection, they do not address the relative contribution of early (C3a, C3b) vs. late (C5a, C5b-9) activated complement components to xenogeneic organ damage. To better understand the role of the terminal complement components (C5a, C5b-9) in hyperacute rejection, an anti-human C5 mAb was developed and tested in an ex vivo model of cardiac xenograft rejection. In vitro studies demonstrated that the anti-C5 mAb effectively blocked C5 cleavage in a dose-dependent manner that resulted in complete inhibition of both C5a and C5b-9 generation. Addn. of anti-C5 mAb to human blood used to perfuse a porcine heart prolonged normal sinus cardiac rhythm from a mean time of 25.2 min in hearts perfused with unmodified blood to 79, 296, or >360 min when anti-C5 mAb was added to the blood at 50 .mu.g/mL, 100 .mu.g/mL, or 200 .mu.g/mL, resp. In these expts., activation of the classical complement pathway was completely inhibited. Hearts perfused with blood contg. the highest concn. of anti-C5 mAb had no histol. evidence of hyperacute rejection and no deposition of C5b-9. These expts. suggest that the activated terminal complement components C5a and C5b-9, but not C3a or C3b, play a major role in tissue damage in the porcine-to-human model of hyperacute rejection. They also suggested that targeted inhibition of terminal complement activation by anti-C5 mAbs may be useful in clin. xenotransplantation.

CC 15-4 (Immunocytochemistry)
 ST cardiac xenotransplant **complement** monoclonal antibody
 IT Swine
 (complement inhibition with an anti-C5 monoclonal antibody prevents acute cardiac tissue injury in an ex vivo model of pig-to-human xenotransplantation)

IT **Complement**

RL: BSU (Biological study, unclassified); BIOL (Biological study)
 (complement inhibition with an anti-C5
 monoclonal antibody prevents acute cardiac tissue injury in an ex
 vivo model of pig-to-human xenotransplantation)

IT Antibodies
 RL: BAC (Biological activity or effector, except adverse); BIOL
 (Biological study)
 (monoclonal, complement inhibition with an anti-
 C5 monoclonal antibody prevents acute cardiac tissue
 injury in an ex vivo model of pig-to-human xenotransplantation)

IT Transplant and Transplantation
 (xeno-, complement inhibition with an anti-C5
 monoclonal antibody prevents acute cardiac tissue injury in an ex
 vivo model of pig-to-human xenotransplantation)

IT Heart
 (xenotransplant, complement inhibition with an anti-
 C5 monoclonal antibody prevents acute cardiac tissue
 injury in an ex vivo model of pig-to-human xenotransplantation)

IT 80295-54-1, Complement C5a
 RL: BSU (Biological study, unclassified); BIOL (Biological study)
 (complement inhibition with an anti-C5
 monoclonal antibody prevents acute cardiac tissue injury in an ex
 vivo model of pig-to-human xenotransplantation)

IT 82986-89-8, Complement C5b-9
 RL: BSU (Biological study, unclassified); BIOL (Biological study)
 (role of complement C5b-9 in acute cardiac tissue
 injury in an ex vivo model of pig-to-human xenotransplantation)

L16 ANSWER 10 OF 12 HCAPLUS COPYRIGHT 1997 ACS
 AN 1995:931533 HCAPLUS
 DN 123:337462
 TI Method for reducing immune and hemostatic dysfunctions during
 extracorporeal circulation
 IN Rollins, Scott A.; Smith, Brian R.; Squinto, Stephen P.
 PA Alexion Pharmaceuticals, Inc., USA; Yale University
 SO PCT Int. Appl., 34 pp.
 CODEN: PIXXD2
 PI WO 9525540 A1 950928
 DS W: AU, CA, JP
 RW: AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE
 AI WO 95-US3614 950322
 PRAI US 94-217391 940323
 DT Patent
 LA English
 AB The use of anti-C5 antibodies to reduce the dysfunction of the
 immune and hemostatic systems assocd. with extracorporeal
 circulation procedures, such as, cardiopulmonary bypass procedures,
 is disclosed. The antibodies have been found to significantly
 reduce complement activation, platelet activation, leukocyte
 activation, and platelet-leukocyte adhesion assocd. with such
 procedures. Demonstrated were anti-C5 monoclonal antibody
 inhibition of complement activity, generation of C3a, prevention of
 the generation of c5b-9, platelet and leukocyte activation and
 adhesion during extracorporeal circulation.

IC ICM A61K039-00
 ICS A61K039-395; C07K016-00; C07K016-18
 CC 15-3 (Immunochemistry)
 ST monoclonal antibody complement C5 extracorporeal
 circulation

IT Circulation
(extracorporeal, monoclonal anti-C5 antibody for
reducing immune and hemostatic dysfunctions during extracorporeal
circulation)

IT Circulation
(extracorporeal, cardiopulmonary bypass, monoclonal anti-
C5 antibody for reducing immune and hemostatic
dysfunctions during extracorporeal circulation)

IT Antibodies
RL: THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(monoclonal, monoclonal anti-C5 antibody for reducing
immune and hemostatic dysfunctions during extracorporeal
circulation)

IT 80295-43-8, **Complement C3b**
RL: BPR (Biological process); BIOL (Biological study); PROC
(Process)
(monoclonal anti-C5 antibody for reducing immune and
hemostatic dysfunctions during extracorporeal circulation)

IT 80295-53-0, **Complement C5** 80295-54-1,
Complement C5a 80295-55-2, **Complement C5b**
RL: BPR (Biological process); BSU (Biological study, unclassified);
BIOL (Biological study); PROC (Process)
(monoclonal anti-C5 antibody for reducing immune and
hemostatic dysfunctions during extracorporeal circulation)

L16 ANSWER 11 OF 12 HCAPLUS COPYRIGHT 1997 ACS
AN 1995:805952 HCAPLUS
DN 123:196481
TI Anti-C5 monoclonal antibody therapy prevents
collagen-induced arthritis and ameliorates established disease
AU Wang, Yi; **Rollins, Scott A.**; Madri, Joseph A.; **Matis,**
Louis A.
CS Immunobiol. Program, Alexion Pharmaceuticals, Inc., New Haven, CT,
06511, USA
SO Proc. Natl. Acad. Sci. U. S. A. (1995), 92(19), 8955-9
CODEN: PNASA6; ISSN: 0027-8424
DT Journal
LA English
AB Activated components of the complement system are potent mediators
of inflammation that may play an important role in numerous disease
states. For example, they have been implicated in the pathogenesis
of inflammatory joint diseases including rheumatoid arthritis (RA).
To target complement activation in immune-mediated joint
inflammation, the authors have utilized monoclonal antibodies (mAbs)
that inhibit the complement cascade at C5, blocking the generation
of the major chemotactic and proinflammatory factors C5a and C5b-9.
In this study, the authors demonstrate the efficacy of a mAb
specific for murine C5 in the treatment of collagen-induced
arthritis, an animal model for RA. The authors show that systemic
administration of the anti-C5 mAb effectively inhibits terminal
complement activation in vivo and prevents the onset of arthritis in
immunized animals. Most important, anti-C5 mAb treatment is also
highly effective in ameliorating established disease. These results
demonstrate a crit. role for activated terminal complement
components not only in the induction but also in the progression of
collagen-induced arthritis and suggest that C5 may be an attractive
therapeutic target in RA.

CC 15-8 (Immunochemistry)
ST arthritis **C5 complement** monoclonal antibody

IT Arthritis
 (anti-C5 complement monoclonal antibody
 therapy prevents collagen-induced arthritis and ameliorates
 established disease)

IT Antibodies
 RL: BAC (Biological activity or effector, except adverse); THU
 (Therapeutic use); BIOL (Biological study); USES (Uses)
 (monoclonal, anti-C5 complement monoclonal
 antibody therapy prevents collagen-induced arthritis and
 ameliorates established disease)

IT Arthritis
 (rheumatoid, anti-C5 complement monoclonal
 antibody therapy prevents collagen-induced arthritis and
 ameliorates established disease)

IT Collagens, biological studies
 RL: BPR (Biological process); BIOL (Biological study); PROC
 (Process)
 (type II, anti-C5 complement monoclonal
 antibody therapy prevents collagen-induced arthritis and
 ameliorates established disease)

IT 80295-53-0, Complement c5
 RL: ADV (Adverse effect, including toxicity); BPR (Biological
 process); BSU (Biological study, unclassified); BIOL (Biological
 study); PROC (Process)
 (anti-C5 complement monoclonal antibody
 therapy prevents collagen-induced arthritis and ameliorates
 established disease)

L16 ANSWER 12 OF 12 HCAPLUS COPYRIGHT 1997 ACS
 AN 1995:727042 HCAPLUS
 DN 123:141260
 TI Rapid expression of an anti-human C5 chimeric Fab
 utilizing a vector that replicates in COS and 293 cells
 AU Evans, Mark J.; Hartman, Sandra L.; Wolff, Dennis W.;
 Rollins, Scott A.; Squinto, Stephen P.
 CS Department of Molecular Development, Alexion Pharmaceuticals, Inc.,
 25 Science Park, New Haven, USA
 SO J. Immunol. Methods (1995), 184(1), 123-38
 CODEN: JIMMBG; ISSN: 0022-1759
 DT Journal
 LA English
 AB Inhibition of complement system activation requires the development
 of sol. nonimmunogenic inhibitors with good tissue penetrating
 abilities that are themselves unable to activate complement.
 Chimeric mouse/human Fabs capable of blocking the activity of
 complement proteins are likely to fulfill these criteria. Several
 monoclonal antibodies that inhibit the activation of the human
 complement system have recently been developed. To examine the
 properties of chimeric Fab derived from these monoclonal antibodies,
 we have developed an expression system which allows the rapid prodn.
 of milligram quantities of chimeric Fab. Both the chimeric light
 chain and the chimeric Fd were co-expressed from the same vector,
 pAPEX-3P. This vector contains the SV40 origin of replication,
 which allows the rapid prodn. of chimeric Fab in COS cells for
 preliminary characterization. Addnl., pAPEX-3P contains the
 Epstein-Barr virus origin of replication and a puromycin selectable
 marker for maintenance as a stable episome in human cell lines. A
 prodn. system consisting of transfected 293-EBNA cells cultured in
 serum free medium followed by protein G-Sepharose chromatog. of the

conditioned medium was found to be sufficient for the rapid prodn. of purified chimeric Fab. Here we have utilized this expression system to demonstrate that an anti-human C5 chimeric Fab was a potent inhibitor of complement activation in both in vitro activation assays and an ex vivo model of complement-mediated tissue damage.

- CC 15-3 (Immunochemistry)
- ST pAPEX3P vector antibody Fab **C5 complement**
- IT Genetic vectors
 - (pAPEX-3P; rapid expression of anti-human **C5** chimeric Fab by pAPEX-3P vector in COS and 293 cells and ex vivo model of **complement**-mediated tissue damage)
- IT Injury
 - (tissue; rapid expression of anti-human **C5** chimeric Fab by pAPEX-3P vector in COS and 293 cells and ex vivo model of **complement**-mediated tissue damage)
- IT Animal cell line
 - (293, rapid expression of anti-human **C5** chimeric Fab by pAPEX-3P vector in COS and 293 cells and ex vivo model of **complement**-mediated tissue damage)
- IT Animal cell line
 - (COS, rapid expression of anti-human **C5** chimeric Fab by pAPEX-3P vector in COS and 293 cells and ex vivo model of **complement**-mediated tissue damage)
- IT Antibodies
 - RL: BOC (Biological occurrence); BPN (Biosynthetic preparation); THU (Therapeutic use); BIOL (Biological study); OCCU (Occurrence); PREP (Preparation); USES (Uses)
 - (monoclonal, Fab; rapid expression of anti-human **C5** chimeric Fab by pAPEX-3P vector in COS and 293 cells and ex vivo model of **complement**-mediated tissue damage)
- IT 80295-53-0, **Complement C5**
 - RL: BSU (Biological study, unclassified); BIOL (Biological study)
 - (rapid expression of anti-human **C5** chimeric Fab by pAPEX-3P vector in COS and 293 cells and ex vivo model of **complement**-mediated tissue damage)